Refine Search

Search Results -

Term	Documents
(3 NOT 4).PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD.	3
(L3 NOT L4).PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD.	3

Database:

US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search:

L5

Refine Search

Recall Text   Clear   Interrupt

Search History

DATE: Wednesday, November 15, 2006   **Purge Queries**   Printable Copy   Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; THES=ASSIGNEE; PLUR=YES; OP=AND			
L5	L3 not L4	3	L5
L4	L3 and (oedema or diarrhia)	7	L4
L3	(porcine or swine) same (FUT1 and polymorphism)	10	L3
L2	Bosworth-Brad-T$.in.	8	L2
L1	Bosworth-Brad.in.	1	L1

END OF SEARCH HISTORY

PALM INTRANET

Inventor Name Search

Enter the first few letters of the Inventor's Last Name.
Additionally, enter the first few letters of the Inventor's First name.

Last Name	First Name	
Vogeli	Peter	Search

To go back use Back button on your browser toolbar.

Back to PALM | ASSIGNMENT | OASIS | Home page

PALM INTRANET

Inventor Name Search

Enter the first few letters of the Inventor's Last Name.
Additionally, enter the first few letters of the Inventor's First name.

Last Name	First Name	
Bosworth	Brad	Search

To go back use Back button on your browser toolbar.

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SCORE Search Results Details for Application 09844268 and Search Result us-09-844-268-12.rge.

This page gives you Search Results detail for the Application 09844268 and Search Result us-09-844-268-12.rge.

start

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                       GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          November 13, 2006, 16:38:38 ; Search time 7441 Seconds
                                             (without alignments)
                                             10905.695 Million cell updates/sec

Title:           US-09-844-268-12
Perfect score:   1269
Sequence:        1 ctcgagccatgtgggtcccc..........actcagaggaaaccctgcag 1269

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying. chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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                 2:  gb_pat:*
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                 9:  gb_un:*
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                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1269	100.0	1269	2	AR360893	AR360893 Sequence
3	1269	100.0	1269	2	AR771735	AR771735 Sequence
4	1269	100.0	1269	2	AX752829	AX752829 Sequence
5	1264.2	99.6	1269	2	AR200399	AR200399 Sequence
6	1261	99.4	1269	14	PIGFTF	L50534 Pig (Sus sc
7	1245.8	98.2	3315	14	U70883	U70883 Sus scrofa
8	1245	98.1	2528	14	AF136896	AF136896 Sus scrof
9	1094.8	86.3	1098	2	AX029029	AX029029 Sequence
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11	864.4	68.1	1867	14	AF394920S2	AF394921 Bos tauru
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23	793.4	62.5	1199	2	AR039078	AR039078 Sequence
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27	790.8	62.3	1136	2	AR039080	AR039080 Sequence
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ALIGNMENTS

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DEFINITION  Methods and compositions to identify swine genetically resistant to
            F18 E coli associated diseases.
ACCESSION   BD085288
VERSION     BD085288.1  GI:22630898
KEYWORDS    JP 2001521401-A/12.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Bosworth,B.T. and Vogeli,P.
  TITLE     Methods and compositions to identify swine genetically resistant to
            F18 E coli associated diseases
  JOURNAL   Patent: JP 2001521401-A 12 06-NOV-2001;
            BIOTECHNOLOGY RESEARCH AND DEVELOPMENT CORP, US DEPARTMENT OF
            AGRICULTURE, SWISS FEDERAL INSTITUTE OF TECHNOLOGY ZURICH
COMMENT     OS   Unidentified
            PN   JP 2001521401-A/12
            PD   06-NOV-2001
            PF   20-MAY-1998 JP 1998550579
            PR   20-MAY-1997 US    60/047181
            PI   BRAD T BOSWORTH,PETER VOGELI
            PC   C12Q1/68,C07K14/47
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Methods and compositions to identify swine genetically  CC
                 resistant to F18 E
            CC   coli associated diseases
            FH   Key                Location/Qualifiers
            FT   CDS                9. .1103.
FEATURES             Location/Qualifiers
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Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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RESULT 2
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LOCUS       AR360893                      1269 bp    DNA      linear    PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6596923.
ACCESSION   AR360893
VERSION     AR360893.1  GI:33768402
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Bosworth,B.T. and Vogeli,P.
  TITLE     Methods and compositions to identify swine genetically resistant to
            F18 E. coli associated diseases
  JOURNAL   Patent: US 6596923-A 12 22-JUL-2003;
            Biotechnology Research & Development Corp., The United States of
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Db        1261 ACCCTGCAG 1269
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DEFINITION  Sequence 12 from patent US 6965022.
ACCESSION   AR771735
VERSION     AR771735.1  GI:83347396
KEYWORDS     .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Bosworth,B.T. and Vogeli,P.
  TITLE     Methods to identify swine genetically resistant to F18 E. coli
            associated diseases
  JOURNAL   Patent: US 6965022-A 12 15-NOV-2005;
            The United States of America as represented by the Secretary of
            Agriculture and Swiss Federal Institute of Technology; Washington,
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FEATURES             Location/Qualifiers
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ORIGIN
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  Best Local Similarity  100.0%;  Pred. No. 0;
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Qy      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy     121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy     181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy     241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy     301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy     361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Db     361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

Qy     421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
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Db    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480

Qy    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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Db    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

Qy    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
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Db    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600

Qy    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCT 780

Qy    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
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Db    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900

Qy    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
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Qy   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
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Db   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
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Db   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140

Qy   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
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Db   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
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Db   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy   1261 ACCCTGCAG 1269
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Db   1261 ACCCTGCAG 1269
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RESULT 4
AX752829

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LOCUS       AX752829                     1269 bp    mRNA      linear   PAT 20-JUN-2003
DEFINITION  Sequence 12 from Patent EP1310570.
ACCESSION   AX752829
VERSION     AX752829.1  GI:32134722
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Bosworth,B.T. and Voegeli,P.
  TITLE     Methods and compositions to identify swine genetically resistant to
            F18 E. coli associated diseases
  JOURNAL   Patent: EP 1310570-A 12 14-MAY-2003;
            Biotechnology Research and Development Corporation (US); U.S.
            Department Of Agriculture (US) ; Swiss Federal Institute of
            Technology Zurich (CH)
FEATURES             Location/Qualifiers
     source          1. .1269
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
     gene            1. .1269
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     CDS             9. .1106
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                     /db_xref="GI:32134723"
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                     HNVVSSPVAIFCLAGTPVHPNASDSCPKHPASFSGTWTIYPDGRFGNQMGQYATLLAL
                     AQLNGRQAFIQPAMHAVLAPVFRITLPVLAPEVDRHAPWRELELHDWMSEDYAHLKEP
                     WLKLTGFPCSWTFFHHLREQIRSEFTLHDHLRQEAQGVLSQFRLPRTGDRPSTFVGVH
                     VRRGDYLRVMPKRWKGVVGDGRYLQQAMDWFRARYEAPVFVVTSNGMEWCRKNIDTSR
                     GDVIFAGDGREAAPARDFALLVQCNHTIMTIGTFGFWAAYLAGGDTIYLANFTLPTSS
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ORIGIN
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   Query Match            100.0%;   Score 1269;  DB 2;  Length 1269;
   Best Local Similarity  100.0%;   Pred. No. 0;
   Matches 1269;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy     121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy     181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy     241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA  300

Qy    301  CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG  360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG  360

Qy    361  CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC  420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC  420

Qy    421  ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA  480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA  480

Qy    481  AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC  540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC  540

Qy    541  GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG  600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG  600

Qy    601  TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC  660
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Db    601  TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC  660

Qy    661  ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG  720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG  720

Qy    721  ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT  780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT  780

Qy    781  TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG  840
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Db    781  TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG  840

Qy    841  ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG  900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG  900

Qy    901  TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG  960
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Db    901  TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG  960

Qy    961  CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA  1020
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Db    961  CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA  1020

Qy    1021  TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC  1080
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC  1080

Qy    1081  CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC  1140
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Db    1081  CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC  1140

Qy    1141  AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG  1200
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy     1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
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Db     1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy     1261 ACCCTGCAG 1269
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Db     1261 ACCCTGCAG 1269
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RESULT 5
AR200399
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LOCUS       AR200399                1269 bp    DNA        linear   PAT 20-APR-2002
DEFINITION  Sequence 1 from patent US 6355859.
ACCESSION   AR200399
VERSION     AR200399.1  GI:20250473
KEYWORDS     .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Bosworth,B., Ridpath,J. and Wiseman,B.
  TITLE     Interactions between genotype and diet in swine that prevent E.
            coli associated intestinal disease
  JOURNAL   Patent: US 6355859-A 1 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .1269
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                     /mol_type="unassigned DNA"
ORIGIN
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  Query Match          99.6%;  Score 1264.2;  DB 2;  Length 1269;
  Best Local Similarity  99.8%;  Pred. No. 9.4e-313;
  Matches 1266;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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Db      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Db      361 CCGTCCTGGCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
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Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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Db      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

Qy      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
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Db      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
            |||||    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ACGGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
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Db      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
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Db      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
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Qy     1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
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Db     1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy     1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
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Qy     1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
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Qy     1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy     1261 ACCCTGCAG 1269
            |||||||||
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Db   1261 ACCCTGCAG 1269

RESULT 6
PIGFTF
LOCUS   PIGFTF   1269 bp   DNA   linear   MAM 27-JUN-1996
DEFINITION Pig (Sus scrofa) alpha1,2 fucosyltransferase gene, complete cds.
ACCESSION   L50534
VERSION   L50534.1 GI:1395136
KEYWORDS   fucosyltransferase; glycosyltransferase.
SOURCE   Sus scrofa (pig)
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 1269)
  AUTHORS   Cohney,S., Mouhtouris,E., McKenzie,I.F. and Sandrin,M.S.
  TITLE   Molecular cloning of the gene coding for pig
            alpha-->2fucosyltransferase
  JOURNAL   Immunogenetics 44 (1), 76-79 (1996)
   PUBMED   8613146
COMMENT   Original source text: Sus scrofa (tissue library: genomic) DNA.
FEATURES   Location/Qualifiers
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                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
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     5'UTR   1. .8
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                     /codon_start=1
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     3'UTR   1107. .1269
ORIGIN

     Query Match   99.4%;   Score 1261;   DB 14;   Length 1269;
     Best Local Similarity   99.6%;   Pred. No. 5.7e-312;
     Matches 1264; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

Qy   1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Db   1 CTGCAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy   61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Qy   121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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Db   121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

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Qy    181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db    181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy    241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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Qy    301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
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Qy    361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Qy    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
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Db    721 ACGGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780

Qy    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
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Db    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
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Qy    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
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Qy   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
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Db   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140

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Qy   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
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Db   1261 ACCCTGCAG 1269
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RESULT 7
U70883

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LOCUS       U70883                  3315 bp    DNA     linear   MAM 12-OCT-2005
DEFINITION  Sus scrofa alpha(1,2)fucosyltransferase (FUT1) gene, complete cds.
ACCESSION   U70883
VERSION     U70883.2  GI:4680729
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 337 to 1844)
  AUTHORS   Meijerink,E., Fries,R., Vogeli,P., Masabanda,J., Wigger,G.,
            Stricker,C., Neuenschwander,S., Bertschinger,H.U. and
            Stranzinger,G.
  TITLE     Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11
            are closely linked to the blood group inhibitor (S) and Escherichia
            coli F18 receptor (ECF18R) loci
  JOURNAL   Mamm. Genome 8 (10), 736-741 (1997)
   PUBMED   9321466
REFERENCE   2  (bases 337 to 1844)
  AUTHORS   Meijerink,E., Fries,R., Voegeli,P. and Stranzinger,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-1996) Animal Science, Swiss Federal Institute of
            Technology, Tannenstrasse 1, Zurich, ZH CH-8092, Switzerland
REFERENCE   3  (bases 1 to 3315)
  AUTHORS   Meijerink,E., Fries,R., Voegeli,P. and Stranzinger,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-1999) Animal Science, Swiss Federal Institute of
            Technology, Tannenstrasse 1, Zurich, ZH CH-8092, Switzerland
  REMARK    Sequence update by submitter
COMMENT     On Apr 26, 1999 this sequence version replaced gi:2558692.
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ORIGIN

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    Best Local Similarity 99.4%;  Pred. No. 3.8e-308;
    Matches 1261;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Db      601 CTGCAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 660

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db      781 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCCTTT 840

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
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Db      901 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 960

Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Db      961 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 1020

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
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Db     1021 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 1080

Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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Db     1081 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 1140

Qy      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
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Db     1141 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 1200

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Db     1201 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 1260

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
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Db     1261 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 1320

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
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Db     1321 ATGGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 1380

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
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Db     1381 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 1440

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
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Db     1441 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 1500

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
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Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
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Db     1561 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1620

Qy     1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
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Db     1621 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1680

Qy     1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
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Qy    1141  AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG  1200
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    1741  AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCCAGTAACTTCCGGAGATGCTGGTGG  1800

Qy    1201  TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA  1260
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Db    1801  TCCTGTAGCA-GCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA  1859

Qy    1261  ACCCTGCAG  1269
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Db    1860  ACCCTGCAG  1868
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RESULT 8
AF136896
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LOCUS       AF136896                2528 bp    mRNA    linear   MAM 27-FEB-2001
DEFINITION  Sus scrofa alpha-1,2-fucosyltransferase (FUT1) mRNA, complete cds.
ACCESSION   AF136896
VERSION     AF136896.1  GI:7328563
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 2528)
  AUTHORS   Meijerink,E., Neuenschwander,S., Fries,R., Dinter,A.,
            Bertschinger,H.U., Stranzinger,G. and Vogeli,P.
  TITLE     A DNA polymorphism influencing alpha(1,2)fucosyltransferase
            activity of the pig FUT1 enzyme determines susceptibility of small
            intestinal epithelium to Escherichia coli F18 adhesion
  JOURNAL   Immunogenetics 52 (1-2), 129-136 (2000)
   PUBMED   11132149
REFERENCE   2  (bases 1 to 2528)
  AUTHORS   Meijerink,E., Neuenschwander,S., Stranzinger,G. and Vogeli,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-1999) Institute of Animal Science, Federal
            Institute of Technology, Tannenstrasse 1, Zurich, CH 8092,
            Switzerland
FEATURES             Location/Qualifiers
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         Query Match            98.1%;   Score 1245;   DB 14;   Length 2528;
         Best Local Similarity  99.5%;   Pred. No. 6.4e-308;
         Matches 1259;  Conservative    0;  Mismatches    5;   Indels    1;  Gaps    1;
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Qy         5 AGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTT 64
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Db        88 AGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTT 147

Qy        65 AGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCT 124
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Db       148 AGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCT 207

Qy       125 GGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGG 184
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Db       208 GGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGG 267

Qy       185 CACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGG 244
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Qy       245 GACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCT 304
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Db       328 GACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCT 387

Qy       305 GCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGT 364
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Qy       365 CCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGC 424
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Qy       425 TCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGA 484
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Db       508 TCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGA 567

Qy       485 GCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGA 544
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Qy       545 GCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACT 604
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Qy       605 GAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGT 664
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Qy       665 GCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGG 724
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Qy       725 CCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGT 784
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Qy    845 GATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCA 904
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Qy    965 TGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTT 1024
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Qy   1205 GTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAAACCC 1264
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Qy   1265 TGCAG 1269
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RESULT 9
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LOCUS       AX029029                1098 bp     DNA        linear    PAT 16-SEP-2000
DEFINITION  Sequence 3 from Patent WO9805768.
ACCESSION   AX029029
VERSION     AX029029.1  GI:10190018
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Mckenzie,I.F. and Sandrin,M.S.
  TITLE     Improved nucleic acids encoding a chimeric glycosyltransferase
  JOURNAL   Patent: WO 9805768-A 3 12-FEB-1998;
            AUSTIN RESEARCH INST (AU) ; MCKENZIE IAN FARQUHAR CAMPBELL (AU) ;
            SANDRIN MAURO SERGIO (AU)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        9 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 68
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Db        1 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 60

Qy       69 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 128
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 120

Qy      129 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACG 188
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Db      121 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACG 180

Qy      189 CCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 248
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 240

Qy      249 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 308
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 300

Qy      309 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTG 368
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Db      301 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTG 360

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Db      361 GCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCT 420

Qy      429 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 488
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Qy      549 ATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTGAGT 608
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Qy      669 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGT 728
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Db      661 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT 720

Qy      729 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 788
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Db      721 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 780

Qy      789 ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 848
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Db    841  TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC  900

Qy    909  AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA  968
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Db    901  AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA  960

Qy    969  GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA  1028
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Db    961  GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA  1020

Qy   1029  CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG  1088
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1089  ATGTTGGCTGGGCCTTGA  1106
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RESULT 10
AC168093/c
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DEFINITION  Bos taurus clone CH240-234F5, WORKING DRAFT SEQUENCE, 18 unordered
            pieces.
ACCESSION   AC168093
VERSION     AC168093.3  GI:85678869
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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REFERENCE   1  (bases 1 to 199471)
  AUTHORS   Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
            Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
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            Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,
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Milosavljevic,A., Minja,E., Morgan,M., Morris,S., Munidasa,M.,
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Okwuonu,G., Okwuonu,K., Parker,D., Pasternak,S., Patel,B.,
Patel,V., Paul,H., Perez,A., Perez,L., Petrosino,J., Pham,T.,
Primus,E., Pu,L.-L., Puazo,M., Qin,X., Quinn,A., Quiroz,J.,
Rabata,D., Rachlin,E., Reigh,R., Ren,Y., Reuter,M., Richards,S.,
Rives,C., Rodriguez,F., Rojas,A., Ruiz,S.J., Sana,M., Sanders,W.,
Santibanez,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y.,
Sisson,I., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R.,
Svatek,A., Taylor,E., Taylor,T., Thomas,N., Thorn,R., Thornton,R.,
Trejos,Z., Usmani,K., Vargo,C., Verduzco,D., Villasana,D., Virk,D.,
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Wei,X., Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R.,
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Zhang,Z., Zhou,J., Weinstock,G. and Gibbs,R.A.

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  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 199471)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-SEP-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 199471)
  AUTHORS   .
  CONSRTM   Bovine Genome Sequencing Consortium
  TITLE .   Direct Submission
  JOURNAL   Submitted (24-JAN-2006) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jan 24, 2006 this sequence version replaced gi:74474967.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: FMZS
                Center clone name: CH240-234F5
            -------------- Summary Statistics
                Assembly program: Atlas 3.0;
                Consensus quality: 191995 bases at least Q40
                Consensus quality: 193265 bases at least Q30
                Consensus quality: 194517 bases at least Q20
                Estimated insert size: 197846; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
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*      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*      43990     47481: contig of 3492 bp in length
*      47482     47531: gap of 50 bp
*      47532     82917: contig of 35386 bp in length
*      82918     82967: gap of 50 bp
*      82968     84638: contig of 1671 bp in length
*      84639     84688: gap of 50 bp
*      84689     94185: contig of 9497 bp in length
*      94186     94235: gap of 50 bp
*      94236    106647: contig of 12412 bp in length
*     106648    106697: gap of 50 bp
*     106698    115377: contig of 8680 bp in length
*     115378    115427: gap of 50 bp
*     115428    155940: contig of 40513 bp in length
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*     155991    165469: contig of 9479 bp in length
*     165470    165519: gap of 50 bp
*     165520    167201: contig of 1682 bp in length
*     167202    167251: gap of 50 bp
*     167252    171689: contig of 4438 bp in length
*     171690    171739: gap of 50 bp
*     171740    182819: contig of 11080 bp in length
*     182820    182869: gap of 50 bp
*     182870    188368: contig of 5499 bp in length
*     188369    188599: gap of 231 bp
*     188600    192002: contig of 3403 bp in length
*     192003    193346: gap of 1344 bp
*     193347    194706: contig of 1360 bp in length
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            gap                     197475. .197574
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Db      81900 CTGCAGCCATGTGGGCTCCCGGCCACCGTCACCTCTGTCTGATCTTCCTGCTAACCTGTG 81841

Qy         61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
              |||| ||    |  |||||||||   |  |  |||  |||||||||  ||||||||||||||
Db      81840 TTTTTGCCTGCGTCTTCTTCCTCCTCATCCACCAAAACCTCTTTCACAGTGGCTTAGACC 81781

Qy        121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATAT̈CTGCCTGG 180
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Db     81420 AGGAGCCCTGGCTGAAGCTCACGGGCTTCCCCTGCTCCTGGACCTTCTTCCATCACCTCC 81361

Qy       541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
             ||||  ||||||||||||||||||| ||||  || || ||||| ||||| ||| |
Db     81360 GGGACCAGATCCGCAGCGAGTTCACCCTACACGAGCATCTGCGGCAGGAGGCGCAGCGTT 81301

Qy       601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
             |||||||  | |||| |  |||||||| || | |||||| ||||||||| ||||| ||||
Db     81300 CACTGAGTGGGCTCCGCTTCCCCCGCACGGGAGGCCGCCCGAGCACCTTTGTGGGTGTCC 81241

Qy       661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
             | ||||||||||||||||| ||.| ||||||||||   | ||||||||| ||||||||| |
Db     81240 ATGTGCGCCGCGGGGACTACCTACAGGTGATGCCCCTCCACTGGAAGGGTGTGGTGGGGG 81181

Qy       721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
             | || |||||||||| ||||||||||||||||||||||||||| || |||||||| |||
Db     81180 ATCGCGCTTACCTCCAACAGGCTATGGACTGGTTCCGGGCCCGGCACAAAGCCCCCATCT 81121

Qy       781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCGGGGGG 840
             |||||||||| ||||||||||||| |||||||||| | ||||| ||||||||||||||||
Db     81120 TTGTGGTCACTAGCAACGGCATGAAGTGGTGCCGGGAAACATTGACACCTCCGGGGGG 81061

Qy       841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
             | |||||||| ||.|| || |||| ||||| |||||| || |||||||||||||||||
Db     81060 ATGTGATCTTCGCCGGAGACGGGCAGGAGGGTGCGCCCAACAAAGACTTTGCGCTGCTCA 81001

Qy       901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
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Db     81000 CACAATGCAACCACACCATCATGACCATTGGCACCTTTGGCTTCTGGGCCGCCTACCTGG 80941

Qy       961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
             |||||||| ||||||||| |||| ||||||||||||||     |||||||||||||||||||
Db     80940 CTGGTGGAGACACCATCTACCTGGCCAACTTCACCCTGCCTGATTCCAGCTTCCTGAAGA 80881

Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
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Db     80880 TCTTTAAACCTGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 80821

Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
             | |||||| |||  |||||| | |||| | | |||| ||||||| |||||||| | ||
Db     80820 CGCTCCA-ATGAAGGCTGAGTCTTG-AGGAACAGGGAGACTTTCTGAAATAGCCT-GATC 80764

Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
             ||   ||||||||    |||| |||| |||||||||     || | | | | ||| ||||
Db     80763 CACGTAGGGCCAATAGTATGCATCTCTGGAAGCCC--AGAAGATTCTAAAAGCTTGTGG 80706

Qy      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
             || || || || | |||||| ||||| ||||| ||||| ||||||| |||| ||| ||
Db     80705 TCTTGCAGGTGG-TCGACACCCATTTCTAGAGTCATTCTAGTTGGCTAGACTTGGAGAAA 80647

Qy      1261 A 1261
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Db     80646 A 80646
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RESULT 11
AF394920S2
LOCUS   AF394920S2   1867 bp   mRNA   linear   MAM 23-SEP-2001
DEFINITION Bos taurus alpha(1-2) fucosyltransferase 1 (fut1) gene, exon 2 and

```
                         complete cds.
         ACCESSION   AF394921
         VERSION     AF394921.1  GI:15723257
         KEYWORDS    .
         SEGMENT     2 of 2
         SOURCE      Bos taurus (cattle)
           ORGANISM  Bos taurus
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                     Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                     Pecora; Bovidae; Bovinae; Bos.
         REFERENCE   1  (bases 1 to 1867)
           AUTHORS   Saunier,K., Barreaud,J.P., Eggen,A., Oriol,R., Leveziel,H.,
                     Julien,R. and Petit,J.-M.
           TITLE     Organization of the Bovine alpha2-Fucosyltransferase Gene Cluster
                     Suggests that the Sec1 Gene Might Have Been Shaped Through a
                     Nonautonomous L1-Retrotransposition Event Within the Same Locus
           JOURNAL   Mol. Biol. Evol. 18 (11) (2001) In press
         REFERENCE   2  (bases 1 to 1867)
           AUTHORS   Saunier,K., Barreaud,J.P., Eggen,A., Oriol,R., Leveziel,H.,
                     Julien,R. and Petit,J.-M.
           TITLE     Direct Submission
           JOURNAL   Submitted (26-JUN-2001) Unite de Genetique Moleculaire Animale,
                     UR1061, Faculte des Sciences, 123, Avenue Albert Thomas, Limoges
                     87060, France
         FEATURES             Location/Qualifiers
              source         1. .1867
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                             /chromosome="18"
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                             /number=2
              CDS            6. .1088
                             /gene="fut1"
                             /codon_start=1
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                     WLKLTGFPCSWTFFHHLRDQIRSEFTLHEHLRQEAQRSLSGLRFPRTGGRPSTFVGVH
                     VRRGDYLQVMPLHWKGVVGDRAYLQQAMDWFRARHKAPIFVVTSNGMKWCRENIDTSR
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         ORIGIN

           Query Match            68.1%;  Score 864.4;  DB 14;  Length 1867;
           Best Local Similarity  83.1%;  Pred. No. 2.5e-210;
           Matches 1044;  Conservative    0;  Mismatches  207;  Indels    6;  Gaps    5;

         Qy         5 AGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTT 64
                      ||||||||||| ||| ||| ||| |||||||||||| |||||||| ||||||||
         Db         2 AGCCATGTGGGCTCCCGGCCACCGTCACCTCTGTCTGATCTTCCTGCTAACCTGTGTTTT 61

         Qy        65 AGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCT 124
                      ||      | ||||||||    | || | ||| |||||||| |||||||||||||||| |
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Db       62 TGCCTGCGTCTTCTTCCTCCTCATCCACCAAAACCTCTTTCACAGTGGCTTAGACCTGTT 121

Qy      125 GGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGG 184
            | ||||||||||| || | ||| ||| ||||||||||| | |||||| | ||
Db      122 CCTGCCGTGTCCAGACCGTANCCGGGTGAGATCCCCCGTGGCCATCCTTTGCCTGTCAGG 181

Qy      185 CACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGG 244
            ||| | | | ||||||| ||| || | ||||||||| |||| |||| || | || ||
Db      182 CACACTGATGAACCCCAATGCCACCTTTACCTGTCCCAGGCATTCTGCTTCTGTCTCAGG 241

Qy      245 GACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCT 304
            || |||||||| |||| | |||||||||||||||||||||||| ||||| ||||||||
Db      242 AACTTGGACTATCGACCCCAAAGGCCGGTTTGGGAACCAGATGGGGCAGTACGCCACGCT 301

Qy      305 GCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGT 364
            | ||||||||| ||||||||| ||||||||||||||||||||||| ||||||||||||||
Db      302 GGTGGCCCTGGCCCAGCTCAATGGCCGCCAGGCCTTCATCCAGCCTCCATGCACGCCGT 361

Qy      365 CCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGC 424
            |||||||||||||||||||||||||||| ||||| || ||||||||||||| ||||| |||||
Db      362 CCTGGCCCCCGTGTTCCGCATCACACTGCCCGTGCTGGCGCCCGAGGTGGACAGACACGC 421

Qy      425 TCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGA 484
            |||||||| ||||||||||||||||| |||||||||| ||||| || |||||||| |||||
Db      422 TCCTTGGCAGGAGCTGGAGCTTCATGACTGGATGTCGGAGGAGTACGCCCACTTGAAGGA 481

Qy      485 GCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGA 544
            |||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||
Db      482 GCCCTGGCTGAAGCTCACGGGCTTCCCCTGCTCCTGGACCTTCTTCCATCACCTCCGGGA 541

Qy      545 GCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACT 604
            ||||||||||||||||||||||| ||||| || || ||||| ||||| ||| ||| |||
Db      542 CCAGATCCGCAGCGAGTTCACCCTACACGAGCATCTGCGGCAGGAGGCGCAGCGTTCACT 601

Qy      605 GAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGT 664
            |||| | ||||| | ||||||||| || | ||||||| ||||||||| ||||| ||||| ||
Db      602 GAGTGGGCTCCGCTTCCCCCGCACGGGAGGCCGCCCGAGCACCTTTGTGGGTGTCCATGT 661

Qy      665 GCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGG 724
            |||||||||||||||| || | ||||||||| | ||||||||| ||||||| || |
Db      662 GCGCCGCGGGGACTACCTACAGGTGATGCCCCTCCACTGGAAGGGTGTGGTGGGGGATCG 721

Qy      725 CCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGT 784
            | ||||||||| ||||||||||||||||||||||||||||| || ||||||||| |||||||
Db      722 CGCTTACCTCCAACAGGCTATGGACTGGTTCCGGGCCCGGCACAAAGCCCCCATCTTTGT 781

Qy      785 GGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGGACGT 844
            |||||| |||||||||||||| |||||||| | | ||||| |||||||||||||||||| ||
Db      782 GGTCACTAGCAACGGCATGAAGTGGTGCCGGGAAAACATTGACACCTCCCGGGGGGATGT 841

Qy      845 GATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCA 904
            |||||| || || || |||| ||||| |||||| || ||||||||||||||||| ||
Db      842 GATCTTCGCCGGAGACGGGCAGGAGGGTGCGCCCAACAAAGACTTTGCGCTGCTCACACA 901

Qy      905 GTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGG 964
            ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      902 ATGCAACCACACCATCATGACCATTGGCACCTTTGGCTTCTGGGCCGCCTACCTGGCTGG 961

Qy      965 TGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTT 1024
            |||||| ||||||||| |||| |||||||||||||| ||||||||||||||||||||||||
Db      962 TGGAGACACCATCTACCTGGCCAACTTCACCCTGCCTGATTCCAGCTTCCTGAAGATCTT 1021
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Qy    1025 TAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACT 1084
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    1022 TAAACCTGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCGCT 1081

Qy    1085 CCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACC 1144
           ||| ||| |||||| | |||| | | | |||| ||||||| ||||||||| | || ||
Db    1082 CCA-ATGAAGGCTGAGTCTTG-AGGAACAGGGAGACTTTCTGAAATAGCCT-GATCCACG 1138

Qy    1145 CAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGGTCCT 1204
           |||||||    ||||   ||||| |||||||||     || | | | | ||| ||||||| |
Db    1139 TAGGGCCAATAGTATGCATCTCTGGAAGCCC--AGAAGATTCTAAAAGCTTGTGGTCTT 1196

Qy    1205 GTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAAA 1261
           | || || | ||||| ||||| ||||| |||||| ||| || |||| ||| |||
Db    1197 GCAGGTGG-TCGACACCCATTTCTAGAGTCATTCTAGTTGTCTAGACTTGGAGAAAA 1252
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RESULT 12
AF186465

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LOCUS       AF186465                1083 bp    DNA    linear    MAM 18-OCT-2000
DEFINITION  Bos taurus alpha(1-2) fucosyltransferase 1 (fut1) gene, complete
            cds.
ACCESSION   AF186465
VERSION     AF186465.1  GI:6409299
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1083)
  AUTHORS   Barreaud,J.P., Saunier,K., Souchaire,J., Delourme,D., Oulmouden,A.,
            Oriol,R., Leveziel,H., Julien,R. and Petit,J.M.
  TITLE     Three bovine alpha2-fucosyltransferase genes encode enzymes that
            preferentially transfer fucose on Galbeta1-3GalNAc acceptor
            substrates
  JOURNAL   Glycobiology 10 (6), 611-621 (2000)
   PUBMED   10814703
REFERENCE   2  (bases 1 to 1083)
  AUTHORS   Saunier,K., Giraud-Delville,C. and Furet,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1999) Departement de Genetique Animale, INRA,
            Laobratoire de Genetique Biochimique et de Cytogenetique, Jouy en
            Josas 78352, France
FEATURES             Location/Qualifiers
     source          1. .1083
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
                     /chromosome="18"
     gene            1. .1083
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                     /product="alpha(1-2) fucosyltransferase 1"
     CDS             1. .1083
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                      WLKLTGFPCSWTFFHHLRDQIRSEFTLHEHLRQEAQRSLSGLRFPRTGGRPSTFVGVH
                      VRRGDYLQVMPLHWKGVVGDRAYLQQAMDWFRARHKAPIFVVTSNGMKWCRENIDTSR
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         ORIGIN

         Query Match              64.9%;   Score 823.6;  DB 14;   Length 1083;
         Best Local Similarity    85.2%;   Pred. No. 7.8e-200;
         Matches  919;  Conservative   0;  Mismatches  160;   Indels   0;  Gaps   0;

Qy         9 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 68
             |||||||  |||  |||  |||  ||||||||||||| ||||||||||   |||||||| ||
Db         1 ATGTGGGCTCCCGGCCACCGTCACCTCTGTCTGATCTTCCTGCTAACCTGTGTTTTTGCC 60

Qy        69 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 128
              | |||||||||     | || | |||  |||||||||| ||||||||||||||||||| |
Db        61 TGCGTCTTCTTCCTCCTCATCCACCAAAACCTCTTTCACAGTGGCTTAGACCTGTTCCTG 120

Qy       129 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACG 188
             | |||||||||||| || |  |||   |||  ||||||||||||| | |||||| | |||||
Db       121 CCGTGTCCAGACCGTANCCGGGTGAGATCCCCCGTGGCCATCCTTTGCCTGTCAGGCACA 180

Qy       189 CCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 248
             | | |  |||||||| |||| ||  | | ||||||||| |||| |||| || | || || ||
Db       181 CTGATGAACCCCAATGCCACCTTTACCTGTCCCAGGCATTCTGCTTCTGTCTCAGGAACT 240

Qy       249 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 308
             ||||||||    ||||   | ||||||||||||||||||||||| ||||| |||||||| ||
Db       241 TGGACTATCGACCCCAAAGGCCGGTTTGGGAACCAGATGGGGCAGTACGCCACGCTGGTG 300

Qy       309 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTG 368
             |||||||| ||||||||| |||||||||||||||||||||||  |||||||||||||||||
Db       301 GCCCTGGCCCAGCTCAATGGCCGCCAGGCCTTCATCCAGCCCTCCATGCACGCCGTCCTG 360

Qy       369 GCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCT 428
             ||||||||||||||||||||| |||||  || |||||||||||||  ||||| |||||||||
Db       361 GCCCCCGTGTTCCGCATCACACTGCCCGTGCTGGCGCCCGAGGTGGACAGACACGCTCCT 420

Qy       429 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 488
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Db       421 TGGCAGGAGCTGGAGCTTCATGACTGGATGTCGGAGGAGTACGCCCACTTGAAGGAGCCC 480

Qy       489 TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG 548
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Db       481 TGGCTGAAGCTCACGGGCTTCCCCTGCTCCTGGACCTTCTTCCATCACCTCCGGGACCAG 540

Qy       549 ATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTGAGT 608
             ||||||||||||||||||||| ||||| || ||  ||||| ||||| ||| | |  |||||||
Db       541 ATCCGCAGCGAGTTCACCCTACACGAGCATCTGCGGCAGGAGGCGCAGCGTTCACTGAGT 600

Qy       609 CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC 668
              | |||| |  |||||||||| |||| ||||||||||||||| ||| |||| ||| ||||||
Db       601 GGGCTCCGCTTCCCCCGCACGGGGAGGCCGCCCGAGCACCTTTGTGGGTGTCCATGTGCGC 660

Qy       669 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGT 728
             |||||||||| || | |  |||||||||||| | |||||||||| |||||||| ||  || |
Db       661 CGCGGGGACTACCTACAGGTGATGCCCCTCCACTGGAAGGGTGTGGTGGGGGATCGCGCT 720
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Qy    729 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCTTTGTGGTC 788
          |||||||| |||||||||||||||||||||||||||   || |||||||||| |||||||||||||
Db    721 TACCTCCAACAGGCTATGGACTGGTTCCGGGCCCGGCACAAAGCCCCCATCTTTGTGGTC 780

Qy    789 ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 848
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Db    781 ACTAGCAACGGCATGAAGTGGTGCCGGGAAAACATTGACACCTCCCGGGGGGATGTGATC 840

Qy    849 TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC 908
          || || || || |||| |||||  ||||||  ||  |||||||||||||||||  || |||
Db    841 TTCGCCGGAGACGGGCAGGAGGGTGCGCCCAACAAAGACTTTGCGCTGCTCACACAATGC 900

Qy    909 AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 968
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db    901 AACCACACCATCATGACCATTGGCACCTTTGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 960

Qy    969 GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA 1028
          || ||||||||| |||| ||||||||||||||||     |||||||||||||||||||||||||||||
Db    961 GACACCATCTACCTGGCCAACTTCACCCTGCCTGATTCCAGCTTCCTGAAGATCTTTAAA 1020

Qy   1029 CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCA 1087
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Db   1021 CCTGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCGCTCCA 1079
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RESULT 13
AR075308

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LOCUS       AR075308                8174 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 5 from patent US 5955347.
ACCESSION   AR075308
VERSION     AR075308.1  GI:10002058
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 8174)
  AUTHORS   Lowe,J.B.
  TITLE     Methods and products for the synthesis of oligosaccharide
            structures on glycoproteins, glycolipids, or as free molecules, and
            for the isolation of cloned genetic sequences that determine these
            structures
  JOURNAL   Patent: US 5955347-A 5 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .8174
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ORIGIN
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  Query Match          63.7%;   Score 808.6;  DB 2;   Length 8174;
  Best Local Similarity  79.6%;   Pred. No. 4.1e-196;
  Matches  993;  Conservative   0;  Mismatches  249;  Indels   5;  Gaps    3;
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Qy      1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
          ||  ||||||||||| |||  |||| || || ||||| |||  |||||||||||||||||||
Db   4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737

Qy     61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
          |  |  | | | ||| ||||||||| |  || ||||||||  ||||       |||| ||| ||
Db   4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCC 4797
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Qy    121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
              ||  |  ||||||||||||||     |  |||||   || | ||  |||||||| |||||||||
Db   4798 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGC 4857

Qy    181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
              |||| ||  ||  |    |||||||||||| |||||||||| |||| ||||| ||| | |
Db   4858 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCT 4917

Qy    241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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Qy    301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
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Qy    361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Qy    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
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Db   5158 GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC 5217

Qy    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
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Qy    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
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Qy    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
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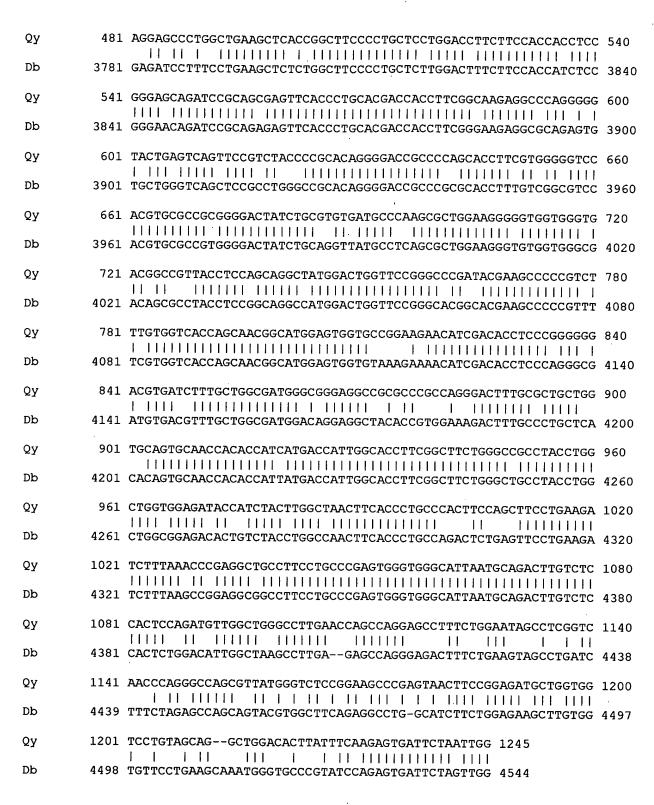
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Db      5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874

Qy      1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
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            RESULT 14
            I34189
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            DEFINITION   Sequence 5 from patent US 5595900.
            ACCESSION    I34189
            VERSION      I34189.1  GI:1824980
            KEYWORDS     .
            SOURCE       Unknown.
              ORGANISM   Unknown.
                         Unclassified.
            REFERENCE    1   (bases 1 to 8174)
              AUTHORS    Lowe,J.B.
              TITLE      Methods and products for the synthesis of oligosaccharide
                         structures on glycoproteins, glycolipids, or as free molecules, and
                         for the isolation of cloned genetic sequences that determine these
                         structures
              JOURNAL    Patent: US 5595900-A 5 21-JAN-1997;
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               Matches  993;  Conservative   0;  Mismatches  249;  Indels   5;  Gaps    3;

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Db    4918 CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA 4977

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Qy     361 CCGTCCTGGCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Qy     541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
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Db    5578 CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 5637

Qy     961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
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Db    5758 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 5815

Qy    1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
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RESULT 15
AY923051

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DEFINITION  Homo sapiens fucosyltransferase 1 (galactoside
            2-alpha-L-fucosyltransferase) (FUT1) gene, complete cds.
ACCESSION   AY923051
VERSION     AY923051.1  GI:58802462
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 8549)
  AUTHORS   Rieder,M.J., Johanson,E.J., da Ponte,S.H., Hastings,N.C.,
            Ahearn,M.O., Bertucci,C.B., Wong,M.W., Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-FEB-2005) Genome Sciences, University of Washington,
            1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI HL66682 Program
            for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.gs.washington.edu).
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Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
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Qy        481  AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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Qy        721  ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
               || ||     ||||||| |||||| |||||||||||||||||||| ||  |||||||||| |
Db       4021  ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT 4080

Qy        781  TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
               | ||||||||||||||||||||||||||||| |    | |||||||||||||||| ||| |
Db       4081  TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCG 4140

Qy        841  ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
               | ||||  |||||||||||||||  | ||||||  | ||    |  |||||||| |||||
Db       4141  ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCA 4200

Qy        901  TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
               |||||||||||||||||||| ||||||||||||||||||||||||||||| ||||||||||
Db       4201  CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 4260

Qy        961  CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
               |||| ||||| || || |||||  |||||||||||||||||| ||         |||||||||
Db       4261  CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGA 4320

Qy       1021  TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
               ||||||| || ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       4321  TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 4380

Qy       1081  CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
               ||||| ||  || ||||| ||||||| ||| |||||| | |||||||  |   |  | | ||
Db       4381  CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 4438

Qy       1141  AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
               | || ||||||  || | | ||  | ||| | | |||| | |  ||||||| ||| |||||
Db       4439  TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 4497

Qy       1201  TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
               | |   | || ||      |||   |   | ||  ||||||||||||| ||||
Db       4498  TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 4544
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Search completed: November 14, 2006, 04:49:39
Job time : 7446 secs

SCORE 1.3   BuildDate: 12/06/2005

SCORE Search Results Details for Application 09844268 and Search Result us-09-844-268-12.rng.

This page gives you Search Results detail for the Application 09844268 and Search Result us-09-844-268-12.rng.

start

```
                         GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          November 13, 2006, 16:38:38 ; Search time 885 Seconds
                                              (without alignments)
                                              9997.495 Million cell updates/sec

Title:           US-09-844-268-12
Perfect score:   1269
Sequence:        1 ctcgagccatgtgggtcccc..........actcagaggaaaccctgcag 1269

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_8:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1269	100.0	1269	2	AAX03811	Aax03811 Swine alp
	2	1269	100.0	1269	2	AAX15872	Aax15872 Fragment
	3	1269	100.0	1269	3	AAZ94417	Aaz94417 Pig alpha
	4	1264.2	99.6	1269	6	AAI72831	Aai72831 FUT1 cDNA
	5	1245.8	98.2	3315	11	ADO58598	Ado58598 Porcine a
	6	1094.8	86.3	1098	2	AAV21640	Aav21640 Pig H tra
	7	808.6	63.7	8174	2	AAQ13332	Aaq13332 GDP-Fuc:b
	8	808.6	63.7	8174	2	AAT61677	Aat61677 Human alp
c	9	808.6	63.7	20001	13	ACN37237	Acn37237 Human per
	10	807	63.6	8174	2	AAQ56908	Aaq56908 DNA encod
	11	806.8	63.6	3373	2	AAT76768	Aat76768 Human alp
	12	806.8	63.6	3373	6	AAD46825	Aad46825 Human alp
	13	794.2	62.6	1174	2	AAT12238	Aat12238 Human H-t
	14	794.2	62.6	1174	3	AAA53820	Aaa53820 Human H-t
	15	792.2	62.4	3791	2	AAT63575	Aat63575 Chicken b
	16	789	62.2	1155	2	AAT01082	Aat01082 2-Alpha-f
	17	789	62.2	1155	2	AAQ98461	Aaq98461 GDP-L-fuc
	18	789	62.2	1155	2	AAT01083	Aat01083 2-Alpha-f
	19	789	62.2	2268	2	AAT63576	Aat63576 Mouse H2K
	20	610.4	48.1	2720	10	ADB53234	Adb53234 Primary r
	21	454.2	35.8	1043	2	AAV29003	Aav29003 Porcine s
	22	454.2	35.8	1043	2	AAV21639	Aav21639 Pig secre
	23	449.4	35.4	3088	6	ABL66311	Abl66311 Lung canc
	24	449.4	35.4	3088	6	ABL70026	Abl70026 Pancreas
	25	449.4	35.4	3088	6	ABL64735	Abl64735 Lung canc
	26	447.8	35.3	2115	2	AAV58323	Aav58323 Human Sec
	27	446.8	35.2	1041	13	ADQ83703	Adq83703 Human tum
	28	446.8	35.2	1041	13	ADQ85849	Adq85849 Human tum
	29	427.8	33.7	2000	12	ADQ83704	Adq83704 Human tum
	30	427.8	33.7	2000	13	ADQ85850	Adq85850 Human tum
	31	423.8	33.4	1068	3	AAC67966	Aac67966 Rat hepat
	32	423.8	33.4	1068	6	AAD27208	Aad27208 Rat hepat
	33	423.8	33.4	1068	8	ABS57887	Abs57887 Rat cDNA
	34	423.8	33.4	1149	3	AAC67965	Aac67965 Rat hepat
	35	423.8	33.4	1149	6	AAD27207	Aad27207 Rat hepat
	36	423.8	33.4	1149	8	ABS57886	Abs57886 Rat cDNA
	37	422.2	33.3	1150	10	ADB97787	Adb97787 Rat cDNA
	38	420.6	33.1	1069	10	ADB97783	Adb97783 Rat cDNA
	39	415.2	32.7	556	12	ACH70096	Ach70096 Human gen
c	40	399	31.4	954	12	ACH89801	Ach89801 Human gen
	41	325.2	25.6	434	12	ACH83796	Ach83796 Human gen
	42	309.4	24.4	1071	2	AAX77268	Aax77268 X. laevis
	43	253	19.9	401	10	ABZ84527	Abz84527 Toxicolog
c	44	129.4	10.2	509	12	ACH76100	Ach76100 Human gen
	45	85.8	6.8	473	3	AAC03536	Aac03536 Human sec

ALIGNMENTS

RESULT 1
AAX03811

```
ID    AAX03811 standard; DNA; 1269 BP.
XX
AC    AAX03811;
XX
DT    01-APR-1999   (first entry)
XX
DE    Swine alpha-1,2-fucosyltransferase 1 encoding DNA.
XX
KW    Swine; pig; alpha-1,2-fucosyltransferase 1; FUT1; resistance;
KW    Escherichia coli; infection; oedema; postweaning diarrhoea;
KW    intestinal disorder; polymorphism; ss.
XX
OS    Sus scrofa.
XX
FH    Key             Location/Qualifiers
FT    CDS             9. .1106
FT                    /*tag=  a
XX
PN    WO9853102-A1.
XX
PD    26-NOV-1998.
XX
PF    20-MAY-1998;    98WO-US010318.
XX
PR    20-MAY-1997;    97US-0047181P.
XX
PA    (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
PA    (USDA ) US SEC OF AGRIC.
PA    (SWTE-) SWISS FEDERAL INST TECHNOLOGY ZURICH.
XX
PI    Bosworth BT,  Vogeli P;
XX
DR    WPI; 1999-059746/05.
DR    P-PSDB; AAW30630.
XX
PT    New method of identifying swine that are resistant to intestinal
PT    colonisation by Escherichia coli - comprises use of genetic polymorphic
PT    markers, used for breeding swine resistant to Escherichia coli-related
PT    diseases.
XX
PS    Claim 6; Fig 1; 35pp; English.
XX
CC    A method has been developed for the identification of swine that are
CC    resistant to intestinal colonisation by E. coli. The method comprises
CC    determining whether a genetic polymorphism associated with resistance to
CC    colonisation is present in a swine sample, and then inferring that the
CC    swine is resistant if it is homozygous for the polymorphism. The method
CC    uses the swine alpha-1,2-fucosyltransferase (FUT1) polymorphism. The
CC    present sequence encodes swine FUT1. The method enables the breeding of
CC    swine that are resistant to E. coli-related diseases. This method
CC    comprises breeding swine that have a genetic polymorphism in the FUT1
CC    gene. More particularly, the identification method identifies swine that
CC    are resistant to E. coli-related intestinal disorders if, in a sample
CC    taken, the only nitrogen base at residue 307 in the FUT1 gene is adenine.
CC    Larger amplified fragments from the assay can be used for RFLP analysis,
CC    and the assay itself is used as a basis for a kit, applied to swine of
CC    any age, in detecting polymorphisms associated with E. coli F18
CC    receptors. The polymorphisms are useful in developing drugs to treat
CC    swine with E. coli-related diseases. However, a mutated form of the
CC    porcine FUT1 gene may interfere with the normal enzyme and prevent it
CC    from producing the intestinal receptor for F18. The detection of
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CC   polymorphic markers in the method disclosed enables the detection and
CC   treatment of E. coli-related intestinal diseases in swine, where there
CC   has been no success using antibiotics due to unsuccessful prophylaxis
XX
SQ   Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 U; 0 Other;
```

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     Query Match              100.0%;   Score 1269;   DB 2;   Length 1269;
     Best Local Similarity    100.0%;   Pred. No. 3.8e-285;
     Matches 1269;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Db        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480

Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

Qy      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||J|||||||||
Db      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
```

```
Qy    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900

Qy    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020

Qy   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140

Qy   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy   1261 ACCCTGCAG 1269
          |||||||||
Db   1261 ACCCTGCAG 1269
```

RESULT 2
AAX15872
ID   AAX15872 standard; DNA; 1269 BP.
XX
AC   AAX15872;
XX
DT   13-MAY-1999 (first entry)
XX
DE   Fragment of pHT83xF encoding swine alpha(1,2) fucosyltransferase.
XX
KW   Swine alpha(1,2) fucosyltransferase; FUT1; Escherichia coli; resistant;
KW   E. coli-associated intestinal disorder; E coli infection; ss.
XX
OS   Synthetic.
OS   Sus sp.
XX
FH   Key   Location/Qualifiers
FT   CDS   9. .1106
FT   /*tag= a
XX
PN   WO9853101-A2.
XX
PD   26-NOV-1998.

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XX
PF   20-MAY-1998;   98WO-US010259.
XX
PR   20-MAY-1997;   97US-0047181P.
XX
PA   (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
XX
PI   Bosworth BT;
XX
DR   WPI; 1999-131692/11.
DR   P-PSDB; AAW97356.
XX
PT   identifying swine genetically resistant to E. coli associated diseases -
PT   using PCR-RFLP to assay for polymorphisms in the alpha(1,2)
PT   fucosyltransferase 1 gene.
XX
PS   Claim 6; Fig 1; 19pp; English.
XX
CC   The present sequence encodes swine alpha(1,2) fucosyltransferase (FUT1).
CC   The specification describes methods relating to Escherichia coli-
CC   resistant swine. One of the methods for identifying a swine resistant to
CC   E. coli-associated intestinal disorders, comprises determining whether
CC   the base at 307 of alpha(1,2) fucosyltransferase1 gene (FUT1) is adenine
CC   (sic), in which case the swine are resistant. The porcine FUT1
CC   polymorphisms can be used to develop drugs for the treatment of swine
CC   having E. coli-associated disease. The methods can also be used in
CC   breeding programmes to identify swine with resistance to E coli infection
XX
SQ   Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 U; 0 Other;
```

Query Match   100.0%;   Score 1269;   DB 2;   Length 1269;
Best Local Similarity   100.0%;   Pred. No. 3.8e-285;
Matches 1269;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy         1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Qy        61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Qy       121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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Db       121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy       181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db       181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy       241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy       301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy       361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
```

```
Qy    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480

Qy    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

Qy    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600

Qy    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCT 780
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Db    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCT 780

Qy    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900

Qy    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020

Qy   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140

Qy   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy   1261 ACCCTGCAG 1269
          |||||||||
Db   1261 ACCCTGCAG 1269
```

RESULT 3
AAZ94417
```
ID   AAZ94417 standard; DNA; 1269 BP.
XX
AC   AAZ94417;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Pig alpha-1-2 fucosyltransferase FUT1 gene.
XX
KW   Alpha-1-2 fucosyltransferase; FUT1; pig; polymorphism; Escherichia coli;
KW   resistance; ss.
XX
OS   Sus scrofa.
XX
FH   Key              Location/Qualifiers
FT   CDS              9. .1106
FT                    /*tag=  a
FT                    /transl_except= (pos:726. .728, aa:Ala)
FT   variation        replace(315,A)
FT                    /*tag=  b
FT                    /note= "adenine is substituted for guanine in resistant
FT                    pigs"
XX
PN   WO200016641-A1.
XX
PD   30-MAR-2000.
XX
PF   17-SEP-1999;   99WO-US021408.
XX
PR   18-SEP-1998;   98US-00151592.
XX
PA   (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Bosworth BT,  Ridpath J,  Wiseman B;
XX
DR   WPI; 2000-283404/24.
DR   P-PSDB; AAY79302.
XX
PT   Improving weight gain in swine using swine genetically resistant
PT   Escherichia coli and feeding swine high levels of plant based protein.
XX
PS   Disclosure; Fig 1; 33pp; English.
XX
CC   This is the nucleotide sequence of the pig FUT1 gene encoding alpha-1-2
CC   fucosyltransferase (see AAY79302). A polymorphism at position 307 of the
CC   coding region is associated with susceptibility to F18 Escherichia coli
CC   colonization; pigs homozygous for adenine at position 307 are resistant
CC   to colonization, while heterozygous animals and animals homozygous for
CC   guanine at position 307 are susceptible to colonization. A claimed method
CC   for improving weight gain in pigs involves selecting animals that are
CC   genetically resistant to E. coli colonization and feeding these animals
CC   high levels of plant-based protein concentrate. A claimed method for
CC   preventing F18 E. coli colonization in swine, especially swine that are
CC   genetically susceptible to F18 E. coli colonization, involves replacing
CC   some or all of the plant-based proteins in the diet with animal-based
CC   proteins. The polymorphism in the FUT1 gene is also useful for developing
CC   drugs to treat swine that have E. coli associated disease. The
CC   polymorphism can be detected using PCR-RFLP tests (see also AAZ94418-19)
```

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XX
SQ    Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 U; 0 Other;

      Query Match            100.0%;   Score 1269;   DB 3;   Length 1269;
      Best Local Similarity  100.0%;   Pred. No. 3.8e-285;
      Matches 1269;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy         1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy        61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy       121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy       181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy       241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy       301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy       361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

Qy       421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480

Qy       481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

Qy       541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGCCCAGGGGG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGCCCAGGGGG 600

Qy       601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy       661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy       721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780

Qy       781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy       841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900

Qy       901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy       961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020

Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140

Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy      1261 ACCCTGCAG 1269
             |||||||||
Db      1261 ACCCTGCAG 1269
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RESULT 4
AAI72831
ID    AAI72831 standard; cDNA; 1269 BP.
XX
AC    AAI72831;
XX
DT    22-JUL-2002   (first entry)
XX
DE    FUT1 cDNA.
XX
KW    Gene; pig; swine; alpha (1,2) fucosyltransferase; FUT1; weight gain; F18;
KW    Escherichia coli; ss.
XX
OS    Sus scrofa.
XX
FH    Key              Location/Qualifiers
FT    CDS              9. .1106
FT                     /*tag=  a
FT                     /product= "FUT1"
FT    mutation         315
FT                     /*tag=  b
FT                     /phenotype= "Confers resistance to F18 E. coli"
XX
PN    US6355859-B1.
XX
PD    12-MAR-2002.
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XX
PF   18-SEP-1998;   98US-00151592.
XX
PR   20-MAY-1997;   97US-0047181P.
XX
PA   (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Bosworth B,  Ridpath J,  Wiseman B;
XX
DR   WPI; 2002-391652/42.
DR   P-PSDB; AAB47995.
XX
PT   Feeding swine genetically susceptible to F18 Escherichia coli
PT   colonization with a low plant protein based diet increases weight gain
PT   and lowers intestinal disease associated with E. coli infection.
XX
PS   Claim 1; Col 13-18; 9pp; English.
XX
CC   This sequence represents the swine alpha (1,2) fucosyltransferase (FUT1)
CC   gene. A FUT1 gene in which there is a base other than adenine at position
CC   307, may be used for improving weight gain in swine that are genetically
CC   susceptible to F18 Escherichia coli. The weight gain may be activated by
CC   feeding a diet of at least 40% animal based proteins. The feeding method
CC   is used to control F18 E. coli associated intestinal disease in swine
XX
SQ   Sequence 1269 BP; 219 A; 414 C; 361 G; 275 T; 0 U; 0 Other;

     Query Match           99.6%;  Score 1264.2;  DB 6;  Length 1269;
     Best Local Similarity  99.8%;  Pred. No. 5e-284;
     Matches 1266;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy       1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy     121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy     181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

Qy     241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy     301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy     361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

Qy     421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480

Qy    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

Qy    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600

Qy    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
          |||||    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACGGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780

Qy    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900

Qy    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020

Qy   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140

Qy   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCCAGTAACTTCCGGAGATGCTGGTGG 1200

Qy   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy   1261 ACCCTGCAG 1269
          |||||||||
Db   1261 ACCCTGCAG 1269
```

RESULT 5

```
AD058598
ID   AD058598 standard; DNA; 3315 BP.
XX
AC   AD058598;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Porcine alpha-1,2-fucosyltransferase (FUT1) DNA.
XX
KW   Detection method; resistance gene; porcine; epidemic diarrhoea;
KW   Escherichia coli F18 receptor; alpha-1; 2-fucosyltransferase; FUT1; pig;
KW   ds.
XX
OS   Sus scrofa.
XX
PN   KR2002080504-A.
XX
PD   26-OCT-2002.
XX
PF   11-APR-2001; 2001KR-00019282.
XX
PR   11-APR-2001; 2001KR-00019282.
XX
PA   (CHOK/) CHO K K.
PA   (CHOI/) CHOI Y J.
PA   (LEES/) LEE S H.
XX
PI   Cho KK,  Choi YJ,  Kim CU,  Lee SH;
XX
DR   WPI; 2003-325954/31.
XX
PT   Detection of resistance gene against porcine epidemic diarrhea.
XX
PS   Disclosure; Fig 1; 12pp; Korean.
XX
CC   The present invention relates to a method of detection of a resistance
CC   gene against porcine epidemic diarrhoea by examining resistance and
CC   susceptibility against Escherichia coli F18 receptor. The detection
CC   involves preparing primers for detecting a mutation of the FUT1 gene, and
CC   detecting a pig, which shows resistance against porcine epidemic
CC   diarrhoea, by PCR using the prepared primers and a test sample collected
CC   from a pig. Also disclosed are sequences of the primers used for the
CC   detection. The present sequence represents porcine FUT1 DNA.
XX
SQ   Sequence 3315 BP; 648 A; 991 C; 901 G; 775 T; 0 U; 0 Other;
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     Query Match             98.2%;  Score 1245.8;  DB 11;  Length 3315;
     Best Local Similarity   99.4%;  Pred. No. 1.2e-279;
     Matches 1261;  Conservative    0;  Mismatches    7;  Indels   1;  Gaps    1;

Qy         1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
             ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTGCAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 660

Qy        61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 720

Qy       121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 780
```

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Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      781 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCCTTT 840

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 900

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 960

Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 1020

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 1080

Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 1140

Qy      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 1200

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 1260

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 1320

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
            | ||||    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 ATGGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 1380

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 1440

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 1500

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 1560

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1620

Qy     1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1680
```

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Qy   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1740

Qy   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1741 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCCAGTAACTTCCGGAGATGCTGGTGG 1800

Qy   1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TCCTGTAGCA-GCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1859

Qy   1261 ACCCTGCAG 1269
          |||||||||
Db   1860 ACCCTGCAG 1868
```

RESULT 6
AAV21640
```
ID   AAV21640 standard; cDNA; 1098 BP.
XX
AC   AAV21640;
XX
DT   08-JUL-1998   (first entry)
XX
DE   Pig H transferase encoding cDNA.
XX
KW   Pig; H transferase; chimeric; glycosyltransferase; gene therapy;
KW   transplantation; ss.
XX
OS   Sus scrofa.
XX
FH   Key               Location/Qualifiers
FT   CDS               1. .1098
FT                     /*tag=  a
FT                     /product= "H transferase"
XX
PN   WO9805768-A1.
XX
PD   12-FEB-1998.
XX
PF   01-AUG-1997;   97WO-AU000492.
XX
PR   02-AUG-1996;   96AU-00001402.
PR   21-AUG-1996;   96US-0024279P.
XX
PA   (AUST-) AUSTIN RES INST.
XX
PI   Mckenzie IFC,  Sandrin MS;
XX
DR   WPI; 1998-159170/14.
DR   P-PSDB; AAW53102.
XX
PT   Nucleic acids encoding chimeric glycosyltransferases - used for altering
PT   carbohydrate levels on the surface of cells, useful in gene therapy and
PT   transplantation.
XX
PS   Example 3; Fig 7; 51pp; English.
XX
CC   The present sequence encodes pig H transferase used in an example of the
CC   present invention. The present invention describes nucleic acids (NA)
```

```
CC    encoding a chimeric glycosyltransferase. The NAs comprise a catalytic
CC    domain of a first glycosyltransferase (GT) and a localisation signal of a
CC    second GT, whereby when the NA is expressed in a cell and where the
CC    chimeric enzyme is located in an area of the cell where it is able to
CC    compete for substrate with a second GT, resulting in reduced levels of a
CC    product from the second GT. The NAs can be used to produce cells and
CC    organs with desired glycosylation patterns. Products and methods of the
CC    present invention can be used to reduce the levels of undesirable
CC    epitopes in cells, tissues or organs which may be used in transplantation
CC    or gene therapy
XX
SQ    Sequence 1098 BP; 181 A; 367 C; 312 G; 238 T; 0 U; 0 Other;
```

```
    Query Match              86.3%;   Score 1094.8;   DB 2;   Length 1098;
    Best Local Similarity    99.8%;   Pred. No. 1.2e-244;
    Matches 1096;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy      9 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 68
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 60

Qy     69 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 128
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 120

Qy    129 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACG 188
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCACG 180

Qy    189 CCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 248
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 240

Qy    249 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 308
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 300

Qy    309 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTG 368
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTG 360

Qy    369 GCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCT 428
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCT 420

Qy    429 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 488
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 480

Qy    489 TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG 548
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG 540

Qy    549 ATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTGAGT 608
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTGAGT 600

Qy    609 CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC 668
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC 660
```

```
Qy    669 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGT 728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    661 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT 720

Qy    729 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 780

Qy    789 ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 840

Qy    849 TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC 900

Qy    909 AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 960

Qy    969 GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA 1020

Qy   1029 CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG 1080

Qy   1089 ATGTTGGCTGGGCCTTGA 1106
          ||||||||||||||||||
Db   1081 ATGTTGGCTGGGCCTTGA 1098
```

RESULT 7
AAQ13332
```
ID    AAQ13332 standard; DNA; 8174 BP.
XX
AC    AAQ13332;
XX
DT    25-MAR-2003   (revised)
DT    07-NOV-1991   (first entry)
XX
DE    GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase gene.
XX
KW    Glycosyltransferase.
XX
OS    Homo sapiens.
XX
FH    Key              Location/Qualifiers
FT    CDS              4686. .5783
FT                     /*tag=  a
XX
PN    WO9112340-A.
XX
PD    22-AUG-1991.
XX
PF    14-FEB-1990;   90US-00479858.
XX
PR    14-FEB-1990;   90US-00479858.
PR    14-FEB-1990;   90US-00480133.
PR    12-DEC-1990;   90US-00627621.
```

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XX
PA    (UNMI ) UNIV MICHIGAN.
XX
PI    Lowe JB;
XX
DR    WPI; 1991-267151/36.
DR    P-PSDB; AAR13751.
XX
PT    Isolation of gene conveying post-translational characteristic - e.g. the
PT    presence of soluble or membrane bound oligo or polysaccharide or
PT  · glycosyltransferase.
XX
PS    Disclosure; Fig 3; 155pp; English.
XX
CC    The DNA encodes a protein sequence capable of functioning as a GDP-
CC    Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The sequence coded by
CC    nucleotides 4782 - 5780 represents the functional protein. The enzyme
CC    produced by the DNA sequence can be used in enzymatic fucosylation of
CC    chain-terminating galactose residues on lactose- amine or neolacto type
CC    beta-D-galactoside to alpha-2-L-fucose residues. See also AAQ13330-
CC    Q13333. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ    Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T; 0 U; 0 Other;
```

```
    Query Match           63.7%;   Score 808.6;  DB 2;   Length 8174;
    Best Local Similarity  79.6%;   Pred. No. 7.7e-178;
    Matches  993;  Conservative      0;  Mismatches 249;  Indels    5;  Gaps    3;
```

```
Qy          1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
              ||  |||||||||| |||  ||||   || || |||| |||  |||||||||||||||||
Db       4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737

Qy         61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
              |  |  | | ||| |||||||||  |  || |||||||||  ||||      |||| ||| ||
Db       4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCC 4797

Qy        121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
              ||  |   |||||||||||||   |  ||||    ||  |  || ||||||||| ||||||||
Db       4798 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGC 4857

Qy        181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
              |||| ||  || |           |||||||||||||  ||||||||||| ||||| |||| | |
Db       4858 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCT 4917

Qy        241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
              |||| |||||||||| |  |||||   |||||||||||| ||  ||||||||||||||||||||
Db       4918 CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA 4977

Qy        301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
              ||||||||||||  ||||| |||||||||||||||||| |||||| ||||| |||||||||||| |
Db       4978 CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG 5037

Qy        361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
              ||| |||||||||| || |||||||||||  ||||| || |||||| || || || |||||| |
Db       5038 CCGCCCTGGCCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCC 5097

Qy        421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
              | |  | || |||||||||||| |||||||||||||||||| ||||| || || |||| | |
Db       5098 GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGA 5157

Qy        481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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                      ||  ||  |   |||||||||||  |  |||||||||||||| |||||  |||||||||||  ||||
Db     5158  GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC  5217

Qy      541  GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG  600
             ||||  ||||||||||  |||||||||||||||||||||||||||  |||||||  |||  | |
Db     5218  GGGAACAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG  5277

Qy      601  TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC  660
             | |||  ||||| ||||  || |   |||||||||||||||||  ||||||| || || ||||
Db     5278  TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCC  5337

Qy      661  ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG  720
             ||||||||||  ||||||||||||||  ||  |||||   ||||||||||||| ||||||||| |
Db     5338  ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG  5397

Qy      721  ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT  780
             ||  ||      |||||||  ||||||  ||||||||||||||||||||  ||  ||||||||||||| |
Db     5398  ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT  5457

Qy      781  TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG  840
             | |||||||||||||||||||||||||||||||||||    | ||||||||||||||||| ||| |
Db     5458  TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCG  5517

Qy      841  ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG  900
             | |||||  ||||||||||||||||||| | ||||||  | ||  |  | ||||||||| |||||
Db     5518  ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCA  5577

Qy      901  TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG  960
             ||||||||||||||||||||  |||||||||||||||||||||||||||||  ||||||||||
Db     5578  CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG  5637

Qy      961  CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA  1020
             |||| |||||| ||  |||||  ||||  ||||||||||||||| ||      ||||||||||
Db     5638  CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGA  5697

Qy     1021  TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC  1080
             |||||||  ||  |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5698  TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC  5757

Qy     1081  CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC  1140
             |||||  || ||  ||||||  |||||||  ||||||  |||||||     ||  |||   |  | ||
Db     5758  CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC  5815

Qy     1141  AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG  1200
             |  || ||||||  || | | || | || ||| | | |||| ||||| |||||  ||| ||||
Db     5816  TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG  5874

Qy     1201  TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG  1245
             | |   | || |||    |   | || ||||||||||| ||||
Db     5875  TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG  5921
```

RESULT 8
AAT61677
ID   AAT61677 standard; DNA; 8174 BP.
XX
AC   AAT61677;
XX
DT   19-JUN-1997   (first entry)
XX
DE   Human alpha(1,2)-fucosyltransferase DNA.

```
      XX
      KW     Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
      KW     blood group H; ss.
      XX
      OS     Homo sapiens.
      XX
      FH     Key             Location/Qualifiers
      FT     CDS             4686. .5783
      FT                     /*tag=  a
      XX
      PN     WO9709421-A1.
      XX
      PD     13-MAR-1997.
      XX
      PF  .  06-SEP-1996;    96WO-US013816.
      XX
      PR     08-SEP-1995;    95US-00525058.
      XX
      PA     (UNMI ) UNIV MICHIGAN.
      XX
      PI     Lowe JB,  Legault DJ;
      XX
      DR     WPI; 1997-192897/17.
      DR     P-PSDB; AAW13640.
      XX
      PT     New recombinant fucosyl:transferase proteins - useful for modifying cell
      PT     surface oligosaccharide structures.
      XX
      PS     Example 1; Page 274-279; 329pp; English.
      XX
      CC     A DNA sequence (AAT61677) codes for human GDP-Fuc:beta-D- galactoside
      CC     alpha(1,2)-fucosyltransferase (AAW13640), an enzyme involved in the
      CC     expression of type I and II blood group H structures. It was obtd. by
      CC     transfecting mouse L cells with DNA derived from human A431 cells, and
      CC     selection of transfectants that expressed the H antigen by using anti-H
      CC     antibody in a panning procedure. The DNA can be used to construct animal
      CC     cell lines with specific capabilities with respect to post-translational
      CC     modification of the oligosaccharides of expressed proteins or lipids, or
      CC     to produce recombinant enzyme for use in oligosaccharide prodn
      XX
      SQ     Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T; 0 U; 0 Other;

         Query Match           63.7%;   Score 808.6;  DB 2;   Length 8174;
         Best Local Similarity  79.6%;  Pred. No. 7.7e-178;
         Matches  993;  Conservative   0;  Mismatches  249;  Indels   5;  Gaps    3;

      Qy         1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
                    ||  ||||||||||| |||  ||||   || || ||||| |||  ||||||||||||||||||||||
      Db      4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737

      Qy        61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
                    |  |   | | ||| ||| |||||||||  |  || ||||||||| ||||      |||| ||| ||
      Db      4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCC 4797

      Qy       121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
                    || |   |||||||||||||||    | |||| || | || |||||||| ||||||||||
      Db      4798 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCAGTGGCCATCTTCTGCCTGC 4857

      Qy       181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
                    |||| ||  || |   ||||||||||||||||| ||||||||||| ||||  ||||| ||| |  | |
      Db      4858 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCT 4917
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```
Qy    241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
          |||| ||||||||| |  ||||||  |||||||||||||| || ||||||||||||||||||
Db   4918 CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA 4977

Qy    301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
          |||||||||| |||||  |||||||||||||||||| |||||| |||| ||||||||||| |
Db   4978 CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG 5037

Qy    361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
          ||| |||||||||| || |||||||||||| ||||| || ||||| || || || |||||| |
Db   5038 CCGCCCTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCC 5097

Qy    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
          | | || ||||||||||||| ||||||||||||||||||||| ||||| || || |||| |
Db   5098 GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGA 5157

Qy    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
          || || |  ||||||||| | ||||||||||||| ||||| ||||||||||||||| |||| 
Db   5158 GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC 5217

Qy    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
          |||| ||||||||||| ||||||||||||||||||||||||||| ||||||| ||| | |
Db   5218 GGGAACAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG 5277

Qy    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
          | |||| ||||| |||| ||  ||||||||||||||||||| ||||||| || || |||
Db   5278 TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCC 5337

Qy    661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
          |||||||||| ||||||||||||||  ||||||  ||||||||||||| ||||||||| |
Db   5338 ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG 5397

Qy    721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
          || ||    |||||||| |||||| |||||||||||||||||  || ||||||||||||| |
Db   5398 ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT 5457

Qy    781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
          | ||||||||||||||||||||||||||||||   | ||||||||||||||||||| || |
Db   5458 TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCG 5517

Qy    841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
          | |||| |||||||||||||||| ||| | |||||  |  ||  |  |||||| |||||
Db   5518 ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCA 5577

Qy    901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
          ||||||||||||||||||| |||||||||||||||||||||||||||||| |||||||||
Db   5578 CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 5637

Qy    961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
          |||| ||||| || ||||| |||| |||||||||||||||    ||  |||||||||||
Db   5638 CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGA 5697

Qy   1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
          ||||||| || |||||  |||||||||||||||||||||||||||||||||||||||||||
Db   5698 TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 5757

Qy   1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
          ||||| ||  |||||||| |||||| ||||||   |  ||| |||  | |   | | || 
Db   5758 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 5815
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Qy   1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
            |  || |||||||  || | | || | || ||| | | | |||| ||||| ||| ||||
Db   5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874

Qy   1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
            | |   | ||    |||    |  | || ||||||||||||| ||||
Db   5875 TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 5921
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RESULT 9
ACN37237/c
ID   ACN37237 standard; DNA; 20001 BP.
XX
AC   ACN37237;
XX
DT   18-NOV-2004   (first entry)
XX
DE   Human periodontal disease related gene FUT1 SEQ ID NO:147.
XX
KW   periodontal disease; polymorphism; ds; human; gene; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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FT   /note= "Variable nucleotide G,A"
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FT   misc_feature   8485
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XX
PN   WO2004042054-A1.
XX
PD   21-MAY-2004.
XX
PF   22-OCT-2003; 2003WO-IB004669.
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XX
PR   23-OCT-2002; 2002JP-00308634.
XX
PA   (HUBI-) HUBIT GENOMIX INC.
PA   (KAMO/) KAMOI K.
XX
PI   Kamoi K, Suzuki A, Numabe Y, Ji G, Muramatsu M, Baba M;
XX
DR   WPI; 2004-400678/37.
XX
PT   Single nucleotide polymorphisms associated with periodontal disease for
PT   examination and assessment of susceptibility to periodontal disease.
XX
PS   Claim 9; SEQ ID NO 147; 0pp; Japanese.
XX
CC   The invention relates to a novel method for examination of periodontal
CC   disease in which genetic polymorphisms are detected in one or more of 51
CC   genes. The method is useful for examination, diagnosis and assessment of
CC   periodontal disease or risk of periodontal disease and the risk of its
CC   progression to severe, aggressive and chronic periodontal disease. The
CC   present sequence represents a polymorphic gene of the invention
XX
SQ   Sequence 20001 BP; 4519 A; 5818 C; 5572 G; 4092 T; 0 U; 0 Other;

     Query Match        63.7%;   Score 808.6;  DB 13;  Length 20001;
     Best Local Similarity  79.6%;   Pred. No. 9.6e-178;
     Matches  993; Conservative  0; Mismatches  249;  Indels  5; Gaps  3;

Qy        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
            ||  ||||||||||| |||  |||| || || ||||| |||  |||||||||||||||||
Db    12792 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 12733

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
            |  |  | |  ||| ||||||||| |  || ||||||||| ||||      |||| ||| ||
Db    12732 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCC 12673

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
            ||  |  |||||||||||||||||||||  |  |||| || | || |||||||| ||||||||
Db    12672 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGC 12613

Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
            ||||  ||  || |    |||||||||||| |||||||||||  || ||||| ||| | |
Db    12612 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCT 12553

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
            ||||  |||||||||| |  ||||| ||||||||||||| || |||||||||||||||||||
Db    12552 CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA 12493

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
            |||||||||| ||||| |||||||||||||||||| |||||| ||||  |||||||||| |
Db    12492 CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG 12433

Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
            ||| ||||||||| || |||||||||||| ||||  || |||| || || || |||| |
Db    12432 CCGCCCTGGCCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCC 12373

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
            | | || |||||||||||||  ||||||||||||||||||| ||||  || || |||| |
Db    12372 GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGA 12313

Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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              ||  || |   ||||||||||| | ||||||||||||| |||||  ||||||||||| ||||
Db    12312 GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCTGCTCTTGGACTTTCTTCCACCATCTCC 12253

Qy      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
            ||||  |||||||||| |||||||||||||||||||||||||  ||||||| ||| |  |
Db    12252 GGGAACAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG 12193

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
            | ||| ||||| |||| ||  ||||||||||||||||||| |||||||| || || ||||
Db    12192 TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCC 12133

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
            |||||||||| |||||||||||||  || ||||| ||||||||||||| ||||||||| |
Db    12132 ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG 12073

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCT 780
              || ||    ||||||| |||||| |||||||||||||||| ||  ||||||||||||| |
Db    12072 ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTT 12013

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
            | ||||||||||||||||||||||||||||||     | ||||||||||||||||| ||| |
Db    12012 TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCG 11953

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
            | |||| |||||||||||||||| || ||||| ||| | |    | ||||||| |||||
Db    11952 ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCA 11893

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
            ||||||||||||||||||| |||||||||||||||||||||||||||| ||||||||||
Db    11892 CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 11833

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
            ||||  |||| ||  |||||  ||||  ||||||||||||||     ||     |||||||||
Db    11832 CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGA 11773

Qy     1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
            ||||||| ||  |||||  ||||||||||||||||||||||||||||||||||||||||||
Db    11772 TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 11713

Qy     1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
            |||||  || |||||||   ||||||| ||  ||||||| || |   |  | | ||
Db    11712 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 11655

Qy     1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
            | ||  |||||| || | | || | || |||  | | | | |||| ||||| ||| ||||
Db    11654 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 11596

Qy     1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
            | |  | ||   |||   |  | ||  |||||||||||| ||||
Db    11595 TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 11549
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RESULT 10
AAQ56908
ID   AAQ56908 standard; DNA; 8174 BP.
XX
AC   AAQ56908;
XX
DT   25-MAR-2003   (revised)
DT   26-JUL-1994   (first entry)
XX

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DE    DNA encoding a glycosyltransferase.
XX
KW    Glycosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell;
KW    surface; oligosaccharide; ss.
XX
OS    Homo sapiens.
XX
FH    Key               Location/Qualifiers
FT    CDS               4686. .5783
FT                      /*tag=  a
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PN    WO9402616-A1.
XX
PD    03-FEB-1994.
XX
PF    20-JUL-1993;    93WO-US006703.
XX
PR    20-JUL-1992;    92US-00914281.
XX
PA    (UNMI ) UNIV MICHIGAN.
XX
PI    Lowe JB;
XX
DR    WPI; 1994-048874/06.
DR    P-PSDB; AAR45936.
XX
PT    DNA fragment encoding a glycosyltransferase - can be used for in vitro
PT    reactions to modify cell surface oligosaccharide(s) e.g. blood gp.
PT    determinants, to protect against transplant rejection.
XX
PS    Disclosure; Fig 3; 249pp; English.
XX
CC    The sequence is that encoding human glycosyl transferase. The enzyme
CC    produced by the DNA may be non glycosylated. This prevents premature loss
CC    of enzyme activity. It can also be used in in vitro reactions to modify
CC    cell surface oligosaccharide mols. e.g. blood group determinants. See
CC    also AAQ56905-12. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ    Sequence 8174 BP; 1628 A; 2228 C; 2322 G; 1996 T; 0 U; 0 Other;
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  Query Match              63.6%;  Score 807;  DB 2;  Length 8174;
  Best Local Similarity    79.6%;  Pred. No. 1.8e-177;
  Matches  992; Conservative    0; Mismatches  250; Indels   5; Gaps   3;
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Qy        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Db     4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
            |  |  | | ||| ||||||||||  |  || |||||||||  ||||     |||| ||| ||
Db     4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCC 4797

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
            || |  ||||||||||||||  | |||| || | || ||||||||| |||||||||
Db     4798 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGC 4857

Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
            |||| ||  || |   ||||||||||||| ||||||||||| |||| ||||| ||| | |
Db     4858 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCT 4917

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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            |||| |||||||||| |  |||||   |||||||||||||| ||  |||||||||||||||||||||
Db    4918  CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA  4977

Qy     301  CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG  360
            |||||||||| |||||  ||||||||||||||||| ||||||  |||| ||||||||||| |
Db    4978  CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG  5037

Qy     361  CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC  420
            |||| |||||||||| ||  |||||||||| ||||| || |||||| || || || |||| |
Db    5038  CCGCCCTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCC  5097

Qy     421  ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA  480
            |  | ||  |||||||||||||| ||||||||||||||||||||||||| |||||  |||| |
Db    5098  GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGA  5157

Qy     481  AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC  540
            || || |  |||||||||| | |||||||||||||| ||||| ||||||||||||| |||
Db    5158  GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC  5217

Qy     541  GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG  600
            |||| |||||||||| |||||||||||||||||||||||||||| |||||||| ||| | |
Db    5218  GGGAACAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG  5277

Qy     601  TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC  660
            | ||| ||||| |||| || ||   |||||||||||||||||| ||||||| || || ||||
Db    5278  TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCC  5337

Qy     661  ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG  720
            |||||||||| |||||||||||||| || |||||  |||||||||||| ||| ||||||| |
Db    5338  ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG  5397

Qy     721  ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT  780
            || || |||||||||||||| |||||||||||||| |  |||||||||||||| | || | |
Db    5398  ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT  5457

Qy     781  TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG  840
            | |||||||||||||||||||||||||||||   |||  | |||||||||||||| ||| |
Db    5458  TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAACATCGACACCTCCCAGGGCG  5517

Qy     841  ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG  900
            | ||||  |||||||||||||| ||||||  | || |  ||| |  ||||| ||| |||||
Db    5518  ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCA  5577

Qy     901  TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG  960
            |||||||||||||||||||| ||||||||||||||||||||||||||||| ||||||||||
Db    5578  CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG  5637

Qy     961  CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA  1020
            |||| |||||| | |||||  |||||||||||||||||||| |     ||  ||||||||||
Db    5638  CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGGCAGACTCTGAGTTCCTGAAGA  5697

Qy    1021  TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC  1080
            |||||| || |||||| || ||||||||||||||||||||||||||||||||||||||||||
Db    5698  TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC  5757

Qy    1081  CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC  1140
            ||||| ||  ||||||||  |||||| |||||  ||  |||||| ||   | | | |  | ||
Db    5758  CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC  5815

Qy    1141  AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG  1200
            |  || ||||||| ||  |  | || | || ||| | | |  |||| ||||| ||| |||
```

```
Db   5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874

Qy   1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
           |  |   | ||     ||| |    | | ||.||||||||||| ||||
Db   5875 TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 5921
```

RESULT 11
AAT76768
ID   AAT76768 standard; cDNA; 3373 BP.
XX
AC   AAT76768;
XX
DT   15-SEP-1997 (first entry)
XX
DE   Human alpha 1,2 fucosyltransferase cDNA.
XX
KW   Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
KW   alpha 1,2 FT; transgene; transgenic mouse; animal model;
KW   intestinal adhesion; Helicobacter pylori infection; stomach;
KW   small intestine; gut; epithelial cell; surface receptor;
KW   carbohydrate antigen; gastritis; peptic ulcer; neoplasia;
KW   gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   104..1201
FT   /*tag= a
FT   /EC_number= "2.4.1.69"
XX
PN   US5625124-A.
XX
PD   29-APR-1997.
XX
PF   11-JUL-1994;   94US-00273411.
XX
PR   11-JUL-1994;   94US-00273411.
XX
PA   (UNIW) UNIV WASHINGTON.
XX
PI   Falk P, Gordon JI;
XX
DR   WPI; 1997-258275/23.
DR   P-PSDB; AAW23805.
XX
PT   Animal model for Helicobacter pylori infection - comprising transgenic
PT   mouse expressing human enzyme promoting intestinal adhesion.
XX
PS   Example 1; Col 17-20; 24pp; English.
XX
CC   A claimed transgenic mouse expresses, in its intestinal epithelial cells,
CC   the enzyme human GDP-L-fucose:beta-D-galactoside 2-alpha-L-
CC   fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose: beta
CC   -D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also called alpha
CC   1,3/4 FT). The enzyme is expressed under the control of a gut epithelial
CC   cell-specific promoter and Helicobacter pylori adheres to the transgenic
CC   cells. The transgenic mouse and intestinal epithelial cells from it are
CC   useful as models for screening compounds for the ability to inhibit
CC   adhesion of H. pylori to gut epithelial cells. The present sequence
CC   encodes human alpha 1,2 FT and was published by Larsen et al.,
```

CC   Proc.Natl.Acad.Sci.USA, 87: 6674-6678 (1990)
XX
SQ   Sequence 3373 BP; 687 A; 925 C; 905 G; 856 T; 0 U; 0 Other;

      Query Match   63.6%;   Score 806.8; DB 2;   Length 3373;
      Best Local Similarity 79.7%;   Pred. No. 1.6e-177;
      Matches 990; Conservative   0; Mismatches 247; Indels   5; Gaps   3;

```
Qy        6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
            |||||||| ||| |||| || || ||||| ||| ||||||||||||||||||||||| |
Db      101 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 160

Qy       66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
            | | ||| |||||||| | || ||||||||| |||| |||| |||| 
Db      161 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 220

Qy      126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
            |||||||||||||    | |||| || | || ||||||||| ||||||||| |||| 
Db      221 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGCCGGGT 280

Qy      186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
            || || |    ||||||||||||| |||||||||| |||| ||||| ||| | ||||| 
Db      281 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 340

Qy      246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
            |||||||| | ||||| ||||||||||||| || |||||||||||||||||||||||||
Db      341 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 400

Qy      306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
            ||||| ||||| |||||||||||||||||| |||||| |||| ||||||||||| |||| |
Db      401 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 460

Qy      366 CTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
            |||||||| || ||||||||||||| ||||| || ||||| || || || |||||| | |
Db      461 CTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 520

Qy      426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
            || ||||||||||||| |||||||||||||||||||| |||| ||| || |||| | ||
Db      521 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 580

Qy      486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG 545
            || | ||||||||| | ||||||||||||| |||| |||||||||||| ||||||||||
Db      581 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 640

Qy      546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGGTACTG 605
            ||||||||||| ||||||||||||||||||||||||||| |||||||| ||| | || |||
Db      641 CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 700

Qy      606 AGTCAGTTCCGTCTACCCCGCACAGGGGACGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
            ||||| |||| || |||||||||||||||||||||| ||||||| || || |||||||||
Db      701 GGTCAGCTCCGCCTGGGCCGCACAGGGGACGCCCGCGCACCTTTGTCGGCGTCCACGTG 760

Qy      666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
            ||||| |||||||||||||| || |||| ||||||||||||||| |||||||| ||| ||
Db      761 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy      726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTG 785
            ||||||| |||||| ||||||||||||||||||| || |||||||||||||| || |||
Db      821 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 880

Qy      786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
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                   IIIIIIIIIIIIIIIIIIIIIIIII     I IIIIIIIIIIIIIIII III II III
Db      881 GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 940

Qy      846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
              I IIIIIIIIIIIIII I IIIIII I II    I IIIIIIII IIIII    III
Db      941 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000

Qy      906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
              IIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIII
Db     1001 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 1060

Qy      966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
              IIIII II IIIII IIII IIIIIIIIIIII  II    IIIIIIIIIIIIIII
Db     1061 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1120

Qy     1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
              II II IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db     1121 AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy     1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
              II IIIIII IIIIIII  IIIIII    II   III   I I II   I
Db     1181 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy     1146 AGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGGTCCTG 1205
              II IIIIII  II I I II I II III I I I IIII IIIII III IIIII  I
Db     1239 AGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGGTGTTC 1297

Qy     1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
              I II   III   I   I II IIIIIIIIIIII IIII
Db     1298 CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339
```

RESULT 12
AAD46825
ID   AAD46825 standard; cDNA; 3373 BP.
XX
AC   AAD46825;
XX
DT   27-JAN-2003   (first entry)
XX
DE   Human alpha(1,2)fucosyltransferase (alpha1,2FT) cDNA.
XX
KW   Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT;
KW   transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   104. .1201
FT   /*tag=   a
FT   /product= "Human alpha1,2FT protein"
XX
PN   WO200274948-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-CA000378.
XX
PR   21-MAR-2001; 2001US-0277811P.
XX

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PA    (GERO-) GERON CORP.
XX
PI    Denning C,  Clark AJ,  Schiff JM;
XX
DR    WPI; 2002-759895/82.
DR    P-PSDB; AAE29226.
XX
PT    Mammalian cells, useful for producing animal tissues with carbohydrate
PT    antigens that are compatible for transplantation into human patients.
XX
PS    Disclosure; Page 35-36; 71pp; English.
XX
CC    The invention relates to animal tissues with carbohydrate antigens that
CC    are compatible for transplantation into human patients. The mammalian
CC    cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC    transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC    fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC    with carbohydrate antigens that are compatible for transplantation into
CC    human patients. The present sequence is human alpha1,2FT cDNA
XX
SQ    Sequence 3373 BP; 687 A; 925 C; 905 G; 856 T; 0 U; 0 Other;
```

```
     Query Match              63.6%;   Score 806.8;  DB 6;   Length 3373;
     Best Local Similarity    79.7%;   Pred. No. 1.6e-177;
     Matches  990;  Conservative      0;  Mismatches  247;  Indels    5;  Gaps    3;
```

```
Qy        6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
            ||||||||| |||  |||| || || ||||| |||  |||||||||||||||||||| |
Db      101 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 160

Qy       66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
            | | ||| |||||||| |  || ||||||||| |||   |||| |||| |||
Db      161 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 220

Qy      126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
            |||||||||||||  | |||| || | || ||||||||| |||||||| |||
Db      221 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGCCGGGT 280

Qy      186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
            ||  || |   ||||||||||||  ||||||||||| |||| |||||  ||| | |||||
Db      281 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 340

Qy      246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
            ||||||||| | ||||| |||||||||||||||| || ||||||||||||||||||||||
Db      341 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 400

Qy      306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
            ||||| ||||| |||||||||||||||||| |||||| ||||| |||||||||| ||| |
Db      401 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 460

Qy      366 CTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
            |||||||| || ||||||||||| ||||| || ||||| || || || ||||| | | |
Db      461 CTGGCCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 520

Qy      426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
            || |||||||||||||| |||||||||||||||||||||| |||||| || || |||| | ||
Db      521 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 580

Qy      486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG 545
            || | |||||||||| | ||||||||||||||||||| ||||| |||||||||| ||||||||
Db      581 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 640
```

```
Qy    546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
          |||||||||| |||||||||||||||||||||||||||| |||||||  ||| | || |||
Db    641 CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 700

Qy    606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
          ||||| |||| ||    |||||||||||||||||| |||||||  || || |||||||||
Db    701 GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCCACGTG 760

Qy    666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
          ||||| |||||||||||| ||  ||||| |||||||||||||| |||||||| ||| ||
Db    761 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy    726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTG 785
          ||||||| ||||||| ||||||||||||||||||||| || |||||||||||| || |||
Db    821 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 880

Qy    786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGGACGTG 845
          |||||||||||||||||||||||||||||     | ||||||||||||||| ||| || |||
Db    881 GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 940

Qy    846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
          |  ||||||||||||||| | |||||| | ||     | ||||||| |||||    |||
Db    941 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000

Qy    906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
          ||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||||||
Db   1001 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 1060

Qy    966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
          ||||| || |||||| |||| ||||||||||||||||  || |||||||||||||||||
Db   1061 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1120

Qy   1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
          || || ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1121 AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy   1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
           ||  |||||| |||||| |||||||  |||||| ||  ||   | | |  | | || |
Db   1181 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy   1146 AGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGGTCCTG 1205
           || |||||| || | | || | || ||| | |  | |||| ||||| ||| ||||| |
Db   1239 AGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGGTGTTC 1297

Qy   1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
           | ||    |||    | | || ||||||||||||| ||||
Db   1298 CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339
```

RESULT 13
AAT12238
```
ID   AAT12238 standard; cDNA to mRNA; 1174 BP.
XX
AC   AAT12238;
XX
DT   08-APR-1996  (first entry)
XX
DE   Human H-transferase cDNA.
XX
KW   H-transferase; xenograft hyperacute rejection; transplantation;
```

```
KW    glycosyltransferase; galactose alpha(1,3) galactose; ds.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             15. .1112
FT                    /*tag=  a
XX
PN    WO9534202-A1.
XX
PD    21-DEC-1995.
XX
PF    14-JUN-1995;   95WO-US007554.
XX
PR .  15-JUN-1994;   94US-00260201.
PR    21-JUL-1994;   94US-00278282.
XX
PA    (ALEX-) ALEXION PHARM INC.
PA    (AUST-) AUSTIN RES INST.
XX
PI    Sandrin MS,  Fodor WL,  Rother RP,  Squinto SP,  Mckenzie IFC;
XX
DR    WPI; 1996-049326/05.
DR    P-PSDB; AAR90572.
XX
PT    Redn. of rejection of xenogeneic cells following transplantation - by
PT    introducing a vector expressing fucosyl:transferase into the cells.
XX
PS    Example 1; Page 45-47; 69pp; English.
XX
CC    A cDNA clone (AAT12238) encoding human H-transferase (AAR90572) was obtd.
CC    from cDNA prepd. from human epidermoid carcinoma cells (ATCC CRL 155 A-
CC    431) by PCR using primers (AAT12240-41) based on H- transferase cDNA 5'
CC    and 3' untranslated regions. The cDNA can be incorporated into vector
CC    APEX-1 (AAT12239) for expression in xenogeneic organs, tissues and cells.
CC    This results in decreased expression of the non-human antigen galactose
CC    alpha(1,3) galactose on the surface of the organs etc. so that hyperacute
CC    rejection is reduced upon transplantation to humans
XX
SQ    Sequence 1174 BP; 202 A; 388 C; 328 G; 256 T; 0 U; 0 Other;

   Query Match            62.6%;  Score 794.2;  DB 2;  Length 1174;
   Best Local Similarity  80.7%;  Pred. No. 1.1e-174;
   Matches  940;  Conservative   0;  Mismatches  223;  Indels   2;  Gaps   1;

Qy      6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
          ||||||||| |||  |||| || || ||||| ||| ||||||||||||||||||||| |
Db     12 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 71

Qy     66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
          |  | ||| |||||||||  |  || |||||||||  ||||    |||| |||| |||| |
Db     72 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 131

Qy    126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
          ||||||||||||||   | |||| || | || ||||||||| |||||||| ||||
Db    132 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGCCGGGT 191

Qy    186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
          ||  || |    ||||||||||||| |||||||||| |||| |||||  ||| | |||||
Db    192 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 251
```

```
Qy    246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
          |||||||| | |||||  |||||||||||| || |||||||||||||||||||||||||||
Db    252 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 311

Qy    306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
          ||||| |||||| ||||||||||||||||| ||||||  |||| ||||||||||| |||| |
Db    312 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 371

Qy    366 CTGGCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
          ||||||||| || |||||||||||| ||||| || ||||| || || || ||||| | | |
Db    372 CTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 431

Qy    426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
          || ||||||||||||| ||||||||||||||||||| |||| || || |||| | | ||
Db    432 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 491

Qy    486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACTCCGGGAG 545
          || |    ||||||||| | |||||||||||| ||||| ||||||||||| ||||||||
Db    492 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 551

Qy    546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
          ||||||||||| ||||||||||||||||||||||||||| |||||||| ||| | || |||
Db    552 CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 611

Qy    606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
          ||||| |||| ||    |||||||||||||||||||||  ||||||| || || ||||||||
Db    612 GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCCACGTG 671

Qy    666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
          ||||| |||||||||||| ||  ||||||  |||||||||||| ||| |||||||| || ||
Db    672 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 731

Qy    726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTG 785
          ||||||| ||||||  ||||||||||||||||||||| || |||||||||||| || |||
Db    732 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 791

Qy    786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
          ||||||||||||||||||||||||||   |    ||||||||||||||||| ||| || |||
Db    792 GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 851

Qy    846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
          |  |||||||||||||||| | |||||| | ||    | |||||||| |||||    |||
Db    852 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 911

Qy    906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
          |||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Db    912 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 971

Qy    966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
           ||||| || ||||| ||||  ||||||||||||||     || |||||||||||||||
Db    972 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1031

Qy   1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
          || || |||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1091

Qy   1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
          ||  ||||||  |||||||  |||||||  ||  ||| | |  || | | || |
Db   1092 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1149

Qy   1146 AGGGCCAGCGTTATGGGTCTCCGGA 1170
```

```
                  ||  ||||||   || |  |  || |  ||
Db        1150 AGAGCCAGCAGTACGTGGCTTCAGA 1174
```

RESULT 14
AAA53820
ID   AAA53820 standard; cDNA to mRNA; 1174 BP.
XX
AC   AAA53820;
XX
DT   03-JAN-2001 (first entry)
XX
DE   Human H-transferase coding sequence.
XX
KW   mesenchymal stem cell; stem cell; H-tranferase; glycosyltransferase;
KW   transplantation; xenotransplantation; transgenic animal; tissue injury;
KW   bone; joint; tendon; ligament; trauma; tumour infection;
KW   muscular dystrophy; osteoarthritis; rheumatoid arthritis; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   15. .1112
FT   /*tag= a
FT   /product= "H-transferase"
XX
PN   WO200049136-A1.
XX
PD   24-AUG-2000.
XX
PF   16-FEB-2000; 2000WO-US003963.
XX
PR   17-FEB-1999;   99US-0120452P.
XX
PA   (USSU) US SURGICAL.
XX
PI   Gruskin EA, Tawil N, Geis D;
XX
DR   WPI; 2000-533106/48.
DR   P-PSDB; AAY97279.
XX
PT   Isolated mesenchymal stem cell comprising nucleic acid encoding an immune
PT   system suppressor polypeptide, useful for treatment of tissue injuries
PT   and/or tissue disorders such as bone and joint fractures.
XX
PS   Example 4; Page 40-41; 60pp; English.
XX
CC   New methods are described for treating a tissue in need of repair or
CC   reconstruction comprising administering a composition comprising a
CC   mesenchymal stem cell where the stem cell differentiates into a cell
CC   which is normally indigenous to the tissue. The mesenchymal stem cell
CC   does not trigger an immune response in the recipient due to it being
CC   transfected with a vector comprising nucleic acid which encodes for an
CC   immune system repressor polypeptide. The mesenchymal stem cell may be
CC   removed from the recepient; transfected and then replaced or derived from
CC   a donor transgenic animal. The transfected mesenchymal stem cells are
CC   useful for treatment of tissue injuries and/or tissue disorders such as
CC   bone and joint fractures, bone defects resulting from trauma, tumour
CC   infection, tendon and ligament defects, congenital defects, muscular
CC   dystrophy, osteoarthritis, and rheumatoid arthritis. The use of the
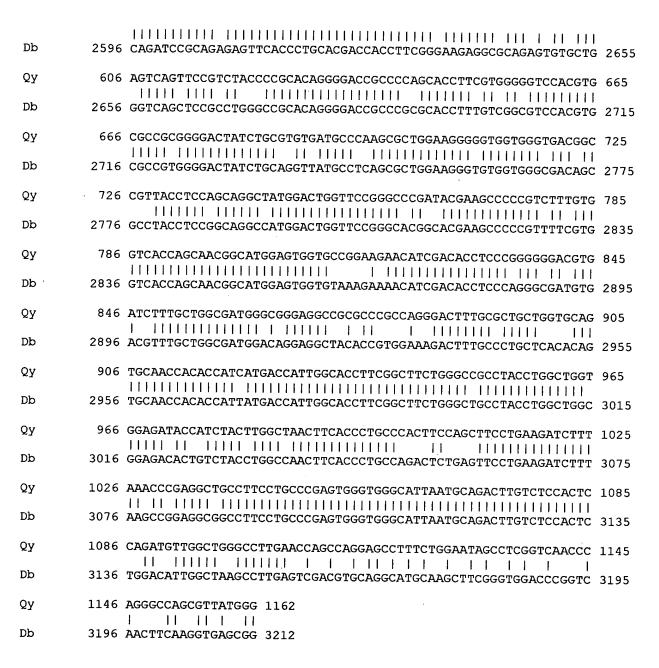CC   genetically engineered cells is advantageous because the need for
```

```
CC   allogenic human donors to provide non-immunogenic cells is eliminated.
CC   Suitable proteins or enzymes that when expressed in xenogenic cells are
CC   capable of reducing the expression of xenogenic antigens and thus reduce
CC   or inhibit rejection of the xenogenic cell when transplanted include
CC   glycosyltransferases such as human alpha-1,2-fucosyltransferase (H-
CC   transferase) and human lysosomal alpha galactosidase
XX
SQ   Sequence 1174 BP; 202 A; 388 C; 328 G; 256 T; 0 U; 0 Other;
```

```
     Query Match            62.6%;   Score 794.2;  DB 3;   Length 1174;
     Best Local Similarity  80.7%;   Pred. No. 1.1e-174;
     Matches  940;  Conservative   0;  Mismatches 223;  Indels   2;  Gaps   1;
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```
Qy        6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
            |||||||||| |||  ||||  || || ||||| ||| |||||||||||||||||||| |
Db       12 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 71

Qy       66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
            | | ||| ||||||||| |  || ||||||||| ||||    |||| ||| ||||| |
Db       72 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 131

Qy      126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
            ||||||||||||||     | |||| || | || ||||||||| |||||||| ||||
Db      132 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGCCGGGT 191

Qy      186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
            ||  || |   |||||||||||||| |||||||||| |||| |||||| ||| | |||||
Db      192 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 251

Qy      246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
            ||||||||| | |||||  ||||||||||||||| || ||||||||||||||||||||||
Db      252 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 311

Qy      306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
            ||||| ||||| ||||||||||||||||| |||||| ||||| |||||||||||| |||| |
Db      312 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 371

Qy      366 CTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
            |||||||| || |||||||||| ||||| || ||||| || || || || |||||| |.| |
Db      372 CTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 431

Qy      426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
            || |||||||||||||| ||||||||||||||||||| ||||| || || |||| | ||
Db      432 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 491

Qy      486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG 545
            || | ||||||||| | |||||||||||||||||||| ||||| ||||||||| ||||||
Db      492 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 551

Qy      546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
            ||||||||||| |||||||||||||||||||||||||||| |||||| ||| | || |||
Db      552 CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 611

Qy      606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
            |||| |||| || ||||||||||||||||||||||| ||||||| || || ||||||||.
Db      612 GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCCACGTG 671

Qy      666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
            ||||| |||||||||||||| || |||||  ||||||||||||| |||||||||| || ||
Db      672 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 731
```

```
Qy    726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTG 785
          ||||||| |||||||  ||||||||||||||||||| ||  |||||||||||| || |||
Db    732 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 791

Qy    786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
          |||||||||||||||||||||||||||||      |  ||||||||||||||||| || |||
Db    792 GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 851

Qy    846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
          |  |||||||||||||||| | |||||| | ||   |  ||||||||| |||||   |||
Db    852 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 911

Qy    906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
          ||||||||||||||| |||||||||||||||||||||||||||||  |||||||||||||
Db    912 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 971

Qy    966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
          ||||| ||  |||||| |||| ||||||||||||||||    ||        |||||||||||
Db    972 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1031

Qy   1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
          || || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1091

Qy   1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
          ||  |||||| |||||||  ||||||  |||||||  ||  |||  |  | |  |
Db   1092 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1149

Qy   1146 AGGGCCAGCGTTATGGGTCTCCGGA 1170
          || ||||||  || | || | ||
Db   1150 AGAGCCAGCAGTACGTGGCTTCAGA 1174
```

RESULT 15
AAT63575
ID   AAT63575 standard; DNA; 3791 BP.
XX
AC   AAT63575;
XX
DT   01-JUL-1997 (first entry)
XX
DE   Chicken beta-actin promoter.
XX
KW   Xenotransplantation; organ transplant; transgenic animal; transgenic pig;
KW   transgenic mouse; antibody mediated rejection; hyperacute rejection;
KW   antigen reducing enzyme; alpha(1,2)fucosyltransferase; beta-actin;
KW   promoter; ss.
XX
OS   Gallus sp.
XX
PN   WO9712035-A2.
XX
PD   03-APR-1997.
XX
PF   23-SEP-1996;   96WO-US015255.
XX
PR   27-SEP-1995;   95US-0004461P.
PR   03-JUL-1996;   96US-00675773.
XX
PA   (NEXT-) NEXTRAN.
XX

```
PI    Diamond LE,  Logan JS,  Byrne GW,  Sharma A;
XX
DR    WPI; 1997-225881/20.
XX
PT    Transgenic animals expressing antigen reducing enzyme and complement
PT    inhibitor - used for production of materials suitable for human
PT    transplantation having a reduced risk of rejection.
XX
PS    Example 6.1; Page 112-115; 146pp; English.
XX
CC    The chicken beta-actin promoter (AAT63575) and the H2Kb gene promoter
CC    (AAT63576) can be utilised in novel vectors for the expression of gal
CC    epitope-reducing enzymes (e.g. human alpha(1,2)fucosyltransferase) and
CC    complement inhibitors (e.g. CD59) on the endothelial cells of transgenic
CC    animals such as pigs and mice. The transgenic animals are used for the
CC    prodn. of materials suitable for transplantation to humans, such
CC    materials being less likely to produce an antibody-mediated rejection
XX
SQ    Sequence 3791 BP; 825 A; 1092 C; 1036 G; 838 T; 0 U; 0 Other;

    Query Match           62.4%;  Score 792.2;  DB 2;  Length 3791;
    Best Local Similarity  80.3%;  Pred. No. 4.2e-174;
    Matches  929;  Conservative   0;  Mismatches 228;  Indels  0;  Gaps  0;

Qy       6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
           ||||||||| |||  |||| || || ||||| ||| ||||||||||||||||||||| |
Db    2056 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 2115

Qy      66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
           | | ||| |||||||| |  || ||||||||| |||  ||||    |||| ||| |||| |
Db    2116 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 2175

Qy     126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
           ||||||||||||||    | |||| || | || ||||||||| |||||||| |||||||| ||||
Db    2176 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGCCGGGT 2235

Qy     186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
           || || |     |||||||||||| |||||||||| ||||| |||||| ||| | |||||
Db    2236 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 2295

Qy     246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
           |||||||| | |||||  ||||||||||||||| || |||||||||||||||||||||||||
Db    2296 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 2355

Qy     306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
           ||||| ||||| ||||||||||||||||| ||||| ||||| |||||||||||| ||||| |
Db    2356 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 2415

Qy     366 CTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
           |||||||| || |||||||||||| ||||| || |||||·|| || || ||||| | | |
Db    2416 CTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 2475

Qy     426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
           || ||||||||||||| ||||||||||||||||||||||||| |||||| || || |||| | ||
Db    2476 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 2535

Qy     486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG 545
           || |  ||||||||| | ||||||||||||||||| ||||| |||||||||||| ||||||||
Db    2536 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 2595

Qy     546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
```

```
                    |||||||||| |||||||||||||||||||||||| ||||||| ||| | || |||
Db    2596 CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 2655

Qy     606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
                    ||||| |||| ||    ||||||||||||||||| ||||||| || || |||||||||
Db    2656 GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCCACGTG 2715

Qy     666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
                    ||||| |||||||||||| || ||||| ||||||||||||| ||||||||| ||| ||
Db    2716 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 2775

Qy     726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCTTTGTG 785
                    |||||| |||||| |||||||||||||||| || ||||||||||| || |||
Db    2776 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTTTCGTG 2835

Qy     786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGGACGTG 845
                    |||||||||||||||||||||||||||    | |||||||||||||||| ||| || |||
Db    2836 GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 2895

Qy     846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
                    |  ||||||||||||||| | ||||||  | ||    |  ||||||| |||||     |||
Db    2896 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 2955

Qy     906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
                    |||||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||
Db    2956 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 3015

Qy     966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
                    ||||| ||  ||||| |||| ||||||||||||    ||        ||||||||||||||
Db    3016 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 3075

Qy    1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
                    || || |||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db    3076 AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 3135

Qy    1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
                    ||  |||||| ||||||   |  |  |  || |  | | |   | | | | |
Db    3136 TGGACATTGGCTAAGCCTTGAGTCGACGTGCAGGCATGCAAGCTTCGGGTGGACCCGGTC 3195

Qy    1146 AGGGCCAGCGTTATGGG 1162
                    |   ||  || |  ||
Db    3196 AACTTCAAGGTGAGCGG 3212
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Search completed: November 14, 2006, 05:04:31
Job time : 890 secs

<div style="border:1px solid">SCORE 1.3   BuildDate: 12/06/2005</div>

SCORE Search Results Details for Application 09 and Search Result us-09-844-268-12.rnpb

This page gives you Search Results detail for the Application 09844268 and Search Result us-09-84

start

Go Bac

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                      GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:           November 13, 2006, 21:00:25 ; Search time 1815 Seconds
                                              (without alignments)
                                              8591.190 Million cell updates/sec

Title:            US-09-844-268-12
Perfect score:    1269
Sequence:         1 ctcgagccatgtgggtcccc.........actcagaggaaaccctgcag 1269

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:       37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_NA_Main:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
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and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	1269	100.0	1269	3	US-09-844-705-12	Sequence 12, Appl
	3	1094.8	86.3	1098	3	US-09-051-034A-3	Sequence 3, Appli
	4	808.6	63.7	8174	3	US-09-863-475A-5	Sequence 5, Appli
	5	806.8	63.6	3373	6	US-10-105-963-9	Sequence 9, Appli
	6	806.8	63.6	3373	16	US-11-219-419-9	Sequence 9, Appli
	7	454.2	35.8	1043	3	US-09-051-034A-1	Sequence 1, Appli
	8	454.2	35.8	1043	3	US-09-254-077A-5	Sequence 5, Appli
	9	449.4	35.4	3088	3	US-09-954-456-45	Sequence 45, Appl
	10	449.4	35.4	3088	3	US-09-954-456-1621	Sequence 1621, Ap
	11	449.4	35.4	3088	3	US-09-969-347-234	Sequence 234, App
	12	449.4	35.4	3088	10	US-10-843-641A-3072	Sequence 3072, Ap
	13	449.4	35.4	3088	10	US-10-843-641A-4648	Sequence 4648, Ap
	14	449.4	35.4	3088	10	US-10-843-641A-8363	Sequence 8363, Ap
	15	449.4	35.4	3088	10	US-10-756-149-275	Sequence 275, App
	16	423.8	33.4	1068	3	US-09-999-672-9	Sequence 9, Appli
	17	423.8	33.4	1068	6	US-10-040-863-9	Sequence 9, Appli
	18	423.8	33.4	1149	3	US-09-999-672-7	Sequence 7, Appli
	19	423.8	33.4	1149	6	US-10-040-863-7	Sequence 7, Appli
	20	415.2	32.7	556	7	US-10-029-386-3291	Sequence 3291, Ap
c	21	399	31.4	954	7	US-10-029-386-22996	Sequence 22996, A
	22	389.6	30.7	1742	16	US-11-136-527-2562	Sequence 2562, Ap
	23	325.2	25.6	434	7	US-10-029-386-16991	Sequence 16991, A
	24	172.6	13.6	607	4	US-09-925-065A-737666	Sequence 737666,
	25	172.6	13.6	607	5	US-09-925-065A-737666	Sequence 737666,
c	26	129.4	10.2	509	7	US-10-029-386-9295	Sequence 9295, Ap
	27	103.6	8.2	600	16	US-11-136-527-6658	Sequence 6658, Ap
c	28	86	6.8	620	4	US-09-925-065A-56199	Sequence 56199, A
c	29	86	6.8	620	5	US-09-925-065A-56199	Sequence 56199, A
c	30	86	6.8	620	12	US-10-301-480-157437	Sequence 157437,
c	31	86	6.8	620	12	US-10-301-480-770846	Sequence 770846,
	32	74.4	5.9	100	3	US-09-999-672-23	Sequence 23, Appl
	33	74.4	5.9	100	3	US-09-999-672-26	Sequence 26, Appl
	34	74.4	5.9	100	6	US-10-040-863-23	Sequence 23, Appl
	35	74.4	5.9	100	6	US-10-040-863-26	Sequence 26, Appl
	36	71.2	5.6	100	3	US-09-999-672-14	Sequence 14, Appl
	37	71.2	5.6	100	3	US-09-999-672-17	Sequence 17, Appl
	38	71.2	5.6	100	6	US-10-040-863-14	Sequence 14, Appl
	39	71.2	5.6	100	6	US-10-040-863-17	Sequence 17, Appl
	40	69.6	5.5	100	3	US-09-999-672-29	Sequence 29, Appl
	41	69.6	5.5	100	6	US-10-040-863-29	Sequence 29, Appl
	42	66.4	5.2	100	3	US-09-999-672-20	Sequence 20, Appl
	43	66.4	5.2	100	6	US-10-040-863-20	Sequence 20, Appl
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	45	48.6	3.8	7788	7	US-10-329-079-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-844-268-12
; Sequence 12, Application US/09844268
; Patent No. US20020129395A1

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;  GENERAL INFORMATION:
;   APPLICANT: BOSWORTH, BRAD
;   APPLICANT: VOGELI, PETER
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
;   TITLE OF INVENTION:  RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
;   FILE REFERENCE: 21419/90368
;   CURRENT APPLICATION NUMBER: US/09/844,268
;   CURRENT FILING DATE:  2001-04-27
;   PRIOR APPLICATION NUMBER: 09/443,766
;   PRIOR FILING DATE: 1999-11-19
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 12
;   LENGTH: 1269
;   TYPE: DNA
;   ORGANISM: Porcine
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9)..(1103)
US-09-844-268-12
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Query Match              100.0%;   Score 1269;   DB 3;   Length 1269;
Best Local Similarity    100.0%;   Pred. No. 0;
Matches 1269;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

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Qy         61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC  120
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Db         61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC  120

Qy        121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG  180
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Db        121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG  180

Qy        181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT  240
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Qy        241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA  300
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Db        241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA  300

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Db        301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG  360

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Qy    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
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Db    601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

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Db   1261 ACCCTGCAG 1269
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RESULT 2
US-09-844-705-12
; Sequence 12, Application US/09844705
; Patent No. US20020133836A1
; GENERAL INFORMATION:
; APPLICANT: BOSWORTH, BRAD
; APPLICANT: VOGELI, PETER
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY

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;   TITLE OF INVENTION:  RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
;   FILE REFERENCE: 21419/90368
;   CURRENT APPLICATION NUMBER: US/09/844,705
;   CURRENT FILING DATE:  2001-04-27
;   PRIOR APPLICATION NUMBER: 09/443,766
;   PRIOR FILING DATE: 1999-11-19
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1269
;   TYPE: DNA
;   ORGANISM: Porcine
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9)..(1103)
US-09-844-705-12
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   Query Match              100.0%;  Score 1269;  DB 3;  Length 1269;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 1269;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Db       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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Db      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240

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Db      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

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Db  1261  ACCCTGCAG  1269
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RESULT 3
US-09-051-034A-3
; Sequence 3, Application US/09051034A
; Patent No. US20010055584A1
; GENERAL INFORMATION:
;  APPLICANT:  MCKENZIE, IAN FARQUHAR CAMPBELL
;  APPLICANT:  SANDRIN, MAURO SERGIO
;  TITLE OF INVENTION:  IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
;  TITLE OF INVENTION:  GLYCOSYLTRANSFERASE
;  FILE REFERENCE:  30562.6USWO
;  CURRENT APPLICATION NUMBER:  US/09/051,034A
;  CURRENT FILING DATE:  1998-03-31
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;   PRIOR APPLICATION NUMBER:  PCT/AU97/00492
;   PRIOR FILING DATE:  1997-08-01
;   PRIOR APPLICATION NUMBER:  60/024,279
;   PRIOR FILING DATE:  1996-08-21
;   PRIOR APPLICATION NUMBER:  PO1402
;   PRIOR FILING DATE:  1996-08-02
;   NUMBER OF SEQ ID NOS:  14
;   SOFTWARE:  PatentIn Ver. 2.1
;   SEQ ID NO 3
;     LENGTH: 1098
;     TYPE: DNA
;     ORGANISM: Sus Domesticus
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (1)..(1098)
US-09-051-034A-3
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     Query Match            86.3%;   Score 1094.8;   DB 3;    Length 1098;
     Best Local Similarity  99.8%;   Pred. No. 8.5e-313;
     Matches 1096;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;
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Db        61 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 120

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Db       241 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 300

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Db       361 GCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCT 420

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Db       421 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 480

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Db    601 CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC 660

Qy    669 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGT 728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    661 CGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT 720

Qy    729 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC 780

Qy    789 ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC 840

Qy    849 TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC 900

Qy    909 AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 960

Qy    969 GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTTAAA 1020

Qy   1029 CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG 1080

Qy   1089 ATGTTGGCTGGGCCTTGA 1106
          ||||||||||||||||||
Db   1081 ATGTTGGCTGGGCCTTGA 1098
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RESULT 4
US-09-863-475A-5
; Sequence 5, Application US/09863475A
; Patent No. US20020102688A1
;   GENERAL INFORMATION:
;   APPLICANT: LOWE, JOHN B.
;   TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;   OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; ;   GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;   OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTUR
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;   P.C.
;   STREET: 1755 Jefferson Davis Highway, Fourth Floor
;   CITY: Arlington
;   STATE: Virginia
;   COUNTRY: U.S.A.
;   ZIP: 22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
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;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/863,475A
;            FILING DATE: 24-May-2001
;            CLASSIFICATION:
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 07/914,281
;            FILING DATE: 20-JUL-1992
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Lavalleye, Jean-Paul M. P.
;            REGISTRATION NUMBER: 31,451
;            REFERENCE/DOCKET NUMBER: 2363-060-55
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703)521-4500
;            TELEFAX: (703)486-2347
;            TELEX: 248855 OPAT UR
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 8174 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: unknown
;            TOPOLOGY: unknown
;        MOLECULE TYPE: DNA (genomic)
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-863-475A-5
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  Query Match          63.7%;   Score 808.6;   DB 3;   Length 8174;
  Best Local Similarity  79.6%;  Pred. No. 5.4e-228;
  Matches  993;  Conservative   0;  Mismatches  249;  Indels   5;  Gaps   3;
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Qy        1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG   60
            ||  ||||||||| |||  ||||  || || ||||| ||| ||||||||||||||||||||
Db     4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737

Qy       61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC  120
            |  |  | | |||  |||||||| |  || ||||||||||  ||||     |||| ||| ||
Db     4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCC 4797

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG  180
            ||  |  |||||||||||||||  | ||||   || | || ||||||||| |||||||||
Db     4798 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGC 4857

Qy      181 CGGGCACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT  240
            |||| || || | |     |||||||||| | ||||||||| ||||| ||||| ||| | |
Db     4858 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCT 4917

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA  300
            |||| |||||||||| |  |||| ||||||||||||||| || |||||||||||||||||
Db     4918 CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA 4977

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG  360
            |||||||||| ||||| ||||||||||||||||||| |||||| |||| |||||||||| |
Db     4978 CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG 5037

Qy      361 CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC  420
            ||| |||||||||| || ||||||||||| |||||| || ||||| || || || |||| |
Db     5038 CCGCCCTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCC 5097

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA  480
            | | || |||||||||||||||| |||||||||||||||| ||||| ||| || ||  ||
Db     5098 GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGA 5157
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Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
                || ||  |  |||||||||| | |||||||||||||||| ||||| |||||||||||| ||||
Db     5158 GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC 5217

Qy      541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGG 600
                |||| ||||||||||| |||||||||||||||||||||||||||| ||||||| ||| | |
Db     5218 GGGAACAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG 5277

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
                | |||  ||||| ||||  ||   |||||||||||||||||| ||||||| || || ||||
Db    ·5278 TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCC 5337

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
                |||||||||| |||||||||||||| || ||||| |||||||||||| ||||||||||| |
Db     5338 ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG 5397

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
                || ||     ||||||| |||||| |||||||||||||||||||| || |||||||||||| |
Db     5398 ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT 5457

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
                | ||||||||||||||||||||||||||||||||     | ||||||||||||||||| ||| |
Db     5458 TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCG 5517

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
                | |||| ||||||||||||||||| | ||||| ||| | ||    |  |||||||| |||||
Db     5518 ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCA 5577

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
                |||||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||||||
Db     5578 CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 5637

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
                |||| |||||| ||  ||||| ||||| |||| ||||||||||||||     ||   |||||||||
Db     5638 CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGA 5697

Qy     1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
                ||||||| || ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     5698 TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 5757

Qy     1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
                |||| || |||||| |||||| ||    ||||||     |||||||     ||   |  | ||
Db     5758 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 5815

Qy     1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
                | || ||||||  || | | || | || ||| | | |  | |||| ||||| ||| |||| ||||
Db     5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874

Qy     1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
                |  |   | ||    |||   |  | ||  |||||||||||| ||||
Db     5875 TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 5921
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RESULT 5
US-10-105-963-9
; Sequence 9, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
;   APPLICANT: Geron Corporation
;   APPLICANT: Denning, Chris

```
;  APPLICANT: Clark, A. John
;  APPLICANT: Schiff, J. Michael
;  TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
;  TITLE OF INVENTION:  Transplantation and a Carbohydrate Determinant Selection Syste
;  TITLE OF INVENTION:  Recombination
;  FILE REFERENCE: 731/002
;  CURRENT APPLICATION NUMBER: US/10/105,963
;  CURRENT FILING DATE:  2002-03-21
;  PRIOR APPLICATION NUMBER: US 60/277,811
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 9
;   LENGTH: 3373
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (104)..(1201)
;   OTHER INFORMATION:
US-10-105-963-9
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   Query Match              63.6%;   Score 806.8;  DB  6;   Length 3373;
   Best Local Similarity    79.7%;   Pred. No. 1.5e-227;
   Matches  990;  Conservative     0;  Mismatches  247;  Indels    5;  Gaps     3;

Qy        6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
            |||||||||| ||| ||||  || || ||||| ||| ||||||||||||||||||||| |
Db      101 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 160

Qy       66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
            | | ||| |||||||||  |  || ||||||||| ||||     |||| ||| |||| |
Db      161 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 220

Qy      126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
            |||||||||||||| | ||||  || | || ||||||||| |||||||| |||||| ||||
Db      221 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCAGTGGCCATCTTCTGCCTGCCGGGT 280

Qy      186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
            ||  || |  |||||||||||||| ||||||||| ||||| ||||| ||| | ||||||
Db      281 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 340

Qy      246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
            ||||||||| |  |||||  |||||||||| ||| |||||||||||||||||||||||||
Db      341 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 400

Qy      306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
            ||||| ||||| ||||||||||||||||||| ||||| |||| ||||||||||| |||| |
Db      401 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 460

Qy      366 CTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
            ||||||| || |||||||||||| ||||| || ||||| || || || |||| | | |
Db      461 CTGGCCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 520

Qy      426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
            || |||||||||||| ||||||||||||||||||||| || |||| || ||  |||| ||
Db      521 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 580

Qy      486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG 545
            || | ||||||||| | |||||||||||||||| ||||||| |||||||| | ||||||
Db      581 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 640
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Qy    546  CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
           |||||||||| |||||||||||||||||||||||||||||| ||||||| ||| | || |||
Db    641  CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 700

Qy    606  AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
           ||||| |||| || |||||||||||||||||||| ||||||| || || |||||||||
Db    701  GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCCACGTG 760

Qy    666  CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
           ||||| |||||||||||| || ||||| ||||||||||||| ||||||| ||| ||
Db    761  CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy    726  CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTG 785
           |||||||| ||||||| ||||||||||||||||||| || ||||||||||||| || |||
Db    821  GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 880

Qy    786  GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
           ||||||||||||||||||||||||||||||     | |||||||||||||||| ||| || |||
Db    881  GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 940

Qy    846  ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
           | .|||||||||||||||| | ||||||| | || | ||||||| ||||| |||
Db    941  ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000

Qy    906  TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
           |||||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||
Db   1001  TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 1060

Qy    966  GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
           ||||| || ||||| |||| |||||||||||||||| || |||||||||||||
Db   1061  GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1120

Qy   1026  AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
           || || ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1121  AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy   1086  CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
           || |||||| ||||||| ||||||| || ||| | || | ||
Db   1181  TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy   1146  AGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGGTCCTG 1205
           || |||||| || | | || | || ||| | | | |||| ||||| ||| ||||| |
Db   1239  AGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGGTGTTC 1297

Qy   1206  TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
           | || ||| | | || |||||||||||| ||||
Db   1298  CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339
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RESULT 6
US-11-219-419-9
; Sequence 9, Application US/11219419
; Publication No. US20060057719A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: CARBOHYDRATE DETERMINANT SELECTION
; FILE REFERENCE: 139/003d

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;   CURRENT APPLICATION NUMBER: US/11/219,419
;   CURRENT FILING DATE:   2005-09-02
;   PRIOR APPLICATION NUMBER: US 60/277,811
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: US 10/105,963
;   PRIOR FILING DATE: 2002-03-21
;   NUMBER OF SEQ ID NOS: 40
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 3373
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (104)..(1201)
US-11-219-419-9
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     Query Match              63.6%;   Score 806.8;   DB 16;   Length 3373;
     Best Local Similarity    79.7%;   Pred. No. 1.5e-227;
     Matches  990;  Conservative    0;  Mismatches  247;   Indels   5;  Gaps    3;

Qy          6 GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA 65
              |||||||||| |||  |||| || || ||||| |||  |||||||||||||||||||| |
Db        101 GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCCTC 160

Qy         66 GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG 125
              | | ||| ||||||||| |  || ||||||||| ||||     |||| ||| |||| |
Db        161 TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGTCG 220

Qy        126 GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC 185
              |||||||||||||    | |||| || | | || |||||||| |||||||| |||| ||||
Db        221 ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCAGTGGCCATCTTCTGCCTGCCGGGT 280

Qy        186 ACGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGG 245
              ||  || |   |||||||||||| |||||||||| ||||||||| |||| ||| | |||||
Db        281 ACTGCGATGGGCCCCAACGCCTCCTCTTCCTGTCCCCAGCACCCTGCTTCCCTCTCCGGC 340

Qy        246 ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG 305
              |||||||||| | |||||| |||||||||||||| || |||||||||||||||||||||||
Db        341 ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG 400

Qy        306 CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTC 365
              ||||| |||||| ||||||||||||||||| |||||| |||| ||||||||||| |||| |
Db        401 CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC 460

Qy        366 CTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCT 425
              |||||||| || |||||||||| |||||| || ||||| || || || || ||||| | ||
Db        461 CTGGCCCCGGTATTCCGCATCACCCTGCCCGTGCTGGCCCCAGAAGTGGACAGCCGCACG 520

Qy        426 CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG 485
              || ||||||||||| |||||||||||||||||||| ||||| || || |||| |  ||
Db        521 CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGCGGACTTGAGAGAT 580

Qy        486 CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG 545
              || |   ||||||||| | ||||||||||||| ||||| |||||||||||| ||||||||
Db        581 CCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA 640

Qy        546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
              |||||||||| | |||||||||||||||||||||||||| |||||||| ||| | || |||
Db        641 CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 700
```

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Qy        606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
              ||||| |||| || |||||||||||||||||||| ||||||| || || ||||||||
Db        701 GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCGGCGTCCACGTG 760

Qy        666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
              ||||| ||||||||||||| || ||||| |||||||||||||| |||||||| ||| ||
Db        761 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy        726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTG 785
              ||||||| |||||| ||||||||||||||||||| || |||||||||||| || |||
Db        821 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 880

Qy        786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
              ||||||||||||||||||||||||||||     | |||||||||||||||| ||| || |||
Db        881 GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 940

Qy        846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
              |  ||||||||||||||| | ||||||  | ||      |  |||||||| ||||||     |||
Db        941 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000

Qy        906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
              ||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||||
Db       1001 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 1060

Qy        966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
              ||||| || ||||| |||| |||||||||||||||||     ||     |||||||||||||
Db       1061 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1120

Qy       1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
              || || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 AAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy       1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
              || |||||| ||||||| ||||||| || ||| | ||  |||    | | || |
Db       1181 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy       1146 AGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGGTCCTG 1205
              || |||||| || | | || | || ||| | | | |||| ||||| ||| ||||| |
Db       1239 AGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGGTGTTC 1297

Qy       1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
              | ||    ||| |   | || |||||||||||| ||||
Db       1298 CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339
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RESULT 7
US-09-051-034A-1
; Sequence 1, Application US/09051034A
; Patent No. US20010055584A1
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
; APPLICANT: SANDRIN, MAURO SERGIO
; TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE
; FILE REFERENCE: 30562.6USWO
; CURRENT APPLICATION NUMBER: US/09/051,034A
; CURRENT FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: PCT/AU97/00492
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 60/024,279
; PRIOR FILING DATE: 1996-08-21

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;   PRIOR APPLICATION NUMBER:  PO1402
;   PRIOR FILING DATE:  1996-08-02
;   NUMBER OF SEQ ID NOS:  14
;   SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1043
;   TYPE: DNA
;   ORGANISM: Sus Domesticus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9)..(1031)
US-09-051-034A-1
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   Query Match            35.8%;   Score 454.2;  DB 3;   Length 1043;
   Best Local Similarity  71.8%;   Pred. No. 2e-123;
   Matches  610;  Conservative   0;  Mismatches 233;  Indels   6;  Gaps    1;

Qy       243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
                 || |   ||†|| ||   |   |      ||||| | ||||||||||||||| |||| |||||
Db       183 GGCATGTGGACGATCAATGCCATCGGCCGCCTGGGGAACCAGATGGGGGAGTACGCCACC 242

Qy       303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
                 |||    || ||||||     | | |||||| || | |||||||||||| ||| | |||||| |
Db       243 CTGTACGCGCTGGCCAGGATGAACGGGCGGCCGGCCTTCATCCCGCCCGAGATGCACAGC 302

Qy       363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
                 ||||||||| | ||| | |||||| || || |||||||       ||       | | |
Db       303 ACGCTGGCCCCCATCTTCAGGATCACCCTCCCGGTCCTGCACGCCAGCACGGCCCGCAGG 362

Qy       423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
                 || |||| | |      | ||  ||||||||||| ||| || |||| |   |
Db       363 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGCGGTACCGCCACATCCCG 422

Qy       483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
                 | |   |   ||  ||||| |||| |||||||||||||||||||||||| |||||||||| ||
Db       423 GGGGAGTACGTGCGCCTCACGGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTGCGC 482

Qy       543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
                 ||||||  | |  |||||||||||||||| ||||| | || | |||||||||||   |
Db       483 ACCGAGATCCTCCGGGAGTTCACCCTGCATAACCACGTGCGCGAGGAGGCCCAGGATTTC 542

Qy       603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
                 ||| |       |||| |      |   ||| ||| || || |||| |||||||||| |||
Db       543 CTGCG------GGGTCTGCGGGTGAACGGGAGCCGACCGAGTACCTACGTGGGGGTGCAC 596

Qy       663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
                 |||||||| ||||||| ||| |||   ||||||||||       |||||||| ||||||| |||
Db       597 GTGCGCCGGGGGGGACTACGTGCACGTGATGCCCAACGTGTGGAAGGGCGTGGTGGCCGAC 656

Qy       723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
                 | || ||||| |||||||| |||||||||||||||||| || |||      |||||||||||
Db       657 CGGCGGTACCTGGAGCAGGCCCTGGACTGGTTCCGGGCTCGCTACCGCTCCCCGTCTTT 716

Qy       783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
                 |||||| |||||||||||||||||||| |||||| ||| | |||||| | |||| || || ||
Db       717 GTGGTCTCCAGCAACGGCATGGCCTGGTGTCGGGAAAACATCAATGCCTCGCGCGGCGAT 776

Qy       843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
                 ||| | |||||| ||| ||||     |||| | | ||||||| ||||| ||||||||| |
Db       777 GTGGTGTTTGCCGGCAATGGCATCGAGGGCTCCCCCGCCAAAGACTTCGCGCTGCTCACG 836
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Qy    903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
          ||||| |||||||||  |||||||||||||||||| |||||  ||||||||||||||| |||
Db    837 CAGTGTAACCACACTGTCATGACCATTGGCACGTTCGGGATCTGGGCCGCCTACCTTGCT 896

Qy    963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
          |||||||| |||||||||| ||||| || | ||| || ||        ||  |||||| || | ||
Db    897 GGTGGAGAGACCATCTACCTGGCCAATTACACGCTCCCGGACTCTCCCTTCCTCAAACTC 956

Qy   1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
          ||||| ||||||||| |||||||||||||||||| | || || | | ||||||| |||| |||
Db    957 TTTAAGCCCGAGGCAGCCTTCCTGCCCGAGTGGATTGGGATCGAGGCAGACCTGTCCCCA 1016

Qy   1083 CTCCAGATG 1091
          ||||  | |
Db   1017 CTCCTTAAG 1025
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RESULT 8
US-09-254-077A-5
; Sequence 5, Application US/09254077A
; Publication No. US20020031494A1
; GENERAL INFORMATION:
; APPLICANT: SANDRIN, MAURO S.
; APPLICANT: MCKENZIE, IAN C. F.
; TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
; FILE REFERENCE: 30562.5USWO
; CURRENT APPLICATION NUMBER: US/09/254,077A
; CURRENT FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: PCT/AU97/00540
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PO 1823
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1043
;   TYPE: DNA
;   ORGANISM: Sus scrofa
US-09-254-077A-5

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  Query Match            35.8%;  Score 454.2;  DB 3;  Length 1043;
  Best Local Similarity  71.8%;  Pred. No. 2e-123;
  Matches  610;  Conservative   0;  Mismatches 233;  Indels   6;  Gaps    1;

Qy    243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
          || | |||||| ||  |  |     ||||| | |||||||||||||||| |||| |||||
Db    183 GGCATGTGGACGATCAATGCCATCGGCCGCCTGGGGAACCAGATGGGGGAGTACGCCACC 242

Qy    303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
          |||    || |||||     | | |||||| || | |||||||||||| ||| | |||||| |
Db    243 CTGTACGCGCTGGCCAGGATGAACGGGCGGCCGGCCTTCATCCCGCCCGAGATGCACAGC 302

Qy    363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
          ||||||||| | |||  | |||||| || || |||||||     ||    | | |
Db    303 ACGCTGGCCCCCATCTTCAGGATCACCCTCCCGGTCCTGCACGCCAGCACGGCCGCAGG 362

Qy    423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
          || |||| | |      | || |||||||||| ||| || | ||||  |   |
Db    363 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGCGGTACCGCCACATCCCG 422

Qy    483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
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                            |  |    |     | |      | | | | |   | | | |   | | | | | | | | | | | | | | | | | | |   | | | | | | | | |   | |
Db      423  GGGGAGTACGTGCGCCTCACGGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTGCGC  482

Qy      543  GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA  602
                            | | | | | | |  |   |   | | | | | | | | | | | | | |    | | | | |  |. | |   |   | | | | | | | | | | |     |
Db      483  ACCGAGATCCTCCGGGAGTTCACCCTGCATAACCACGTGCGCGAGGAGGCCCAGGATTTC  542

Qy      603  CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC  662
                            | | |  |              | | | |  |           |     | | |     | | |   | |   | |   | | | |   | | | | | | | | |   | | |
Db      543  CTGCG------GGGTCTGCGGGTGAACGGGAGCCGACCGAGTACCTACGTGGGGGTGCAC  596

Qy      663  GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC  722
                            | | | | | | | |   | | | | | | | |    | | |    | | | | | | | | | | |       | | | | | | | |   | | | | | | |     | | |
Db      597  GTGCGCCGGGGGGGACTACGTGCACGTGATGCCCAACGTGTGGAAGGGCGTGGTGGCCGAC  656

Qy      723  GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT  782
                            |  | |   | | | | |     | | | | | | |     | | | | | | | | | | | | | | | | | |   | |   | | |          | | | | | | | | | | |
Db      657  CGGCGGTACCTGGAGCAGGCCCTGGACTGGTTCCGGGCTCGCTACCGCTCCCCCGTCTTT  716

Qy      783  GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC  842
                            | | | | | |   | | | | | | | | | | | | | | | |     | | | | |   | | |   |   | | | | | | |   |     | | | |   | |   | |   | |
Db      717  GTGGTCTCCAGCAACGGCATGGCCTGGTGTCGGGAAAACATCAATGCCTCGCGCGGCGAT  776

Qy      843  GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG  902
                            | | |  |   | | | | | |  | | |   | | | |      | | | |  | |  | | | | | | | |    | | | | |   | | | | | | | | |      |
Db      777  GTGGTGTTTGCCGGCAATGGCATCGAGGGCTCCCCCGCCAAAGACTTCGCGCTGCTCACG  836

Qy      903  CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT  962
                            | | | | |   | | | | | | | |     | | | | | | | | | | | | | | | |   | | | | |     | | | | | | | | | | | | | | | | |  | | |
Db      837  CAGTGTAACCACACTGTCATGACCATTGGCACGTTCGGGATCTGGGCCGCCTACCTTGCT  896

Qy      963  GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC  1022
                            | | | | | | | |   | | | | | | | | | |   | | | |   | |   |   | | |   | |   | |         | |     | | | | | |   | |     | |
Db      897  GGTGGAGAGACCATCTACCTGGCCAATTACACGCTCCCGGACTCTCCCTTCCTCAAACTC  956

Qy      1023  TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA  1082
                             | | | | |   | | | | | | | | |   | | | | | | | | | | | | | | | | | | |   |   | |   | |     |   | | | | | |   | | | |   | | |
Db      957  TTTAAGCCCGAGGCAGCCTTCCTGCCCGAGTGGATTGGGATCGAGGCAGACCTGTCCCCA  1016

Qy      1083  CTCCAGATG  1091
                             | | | |    |  |
Db      1017  CTCCTTAAG  1025
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RESULT 9
US-09-954-456-45
; Sequence 45, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;   APPLICANT: Young, Paul
;   TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca
;   TITLE OF INVENTION: Sets
;   FILE REFERENCE: 689290-76
;   CURRENT APPLICATION NUMBER: US/09/954,456
;   CURRENT FILING DATE: 2001-09-18
;   PRIOR APPLICATION NUMBER: US/60/233,617
;   PRIOR FILING DATE: 2000-09-18
;   PRIOR APPLICATION NUMBER: US/60/234,052
;   PRIOR FILING DATE: 2000-09-20
;   PRIOR APPLICATION NUMBER: US/60/234,923
;   PRIOR FILING DATE: 2000-09-25

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;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
;   LENGTH: 3088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-45

  Query Match              35.4%;   Score 449.4;  DB 3;   Length 3088;
  Best Local Similarity    71.5%;   Pred. No. 6.8e-122;
  Matches  607;  Conservative     0;  Mismatches  236;  Indels   6;  Gaps    1;

Qy        243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
              |||| |||||| || |   |   ||||| | ||||||||||||| |||| |||||
Db        295 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy        303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
              |||    ||||||||| || | ||||| || |  |||||||||| | |    ||||||| |
Db        355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy        363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
              |||||||||| | ||| | ||||| ||||| || ||        ||        | |||
Db        415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy        423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
              || |||| | |      | || |||||||||||     ||||| ||    ||||||   |
Db        475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy        483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
              | |   |   |     |||||||||| ||||||||||||||||||||||||||||||||||
Db        535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy        543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
              || ||||||| |   |||||||||||||||||||||| | ||| | ||||||||| | |
Db        595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy        603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
              ||| |        | || |     |   ||| || || |||||||| || ||||||||||
Db        655 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy        663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
              || ||||| ||||||||| | | ||| ||||| ||      |||||||||||||||| |||
Db        709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy        723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
              | || ||||| ||||||||| || ||||||||||||| || || ||   ||| | ||||
Db        769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828
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Qy    783  GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC  842
           |||||||||| || ||||||| ||||| ||| ||||||| |||||||||| || ||
Db    829  GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACGGTGAT  888

Qy    843  GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG  902
           ||| | |||||||||||||||    |||| | | || |||| || ||||| || ||
Db    889  GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA  948

Qy    903  CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT  962
           ||||| ||||||||||||||||||||||||| || |||||| |||||||||| ||||| |
Db    949  CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG  1008

Qy    963  GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC  1022
           || |||||| |||||||||| ||||| || | |||||| |||     ||| ||||| || |||
Db   1009  GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC  1068

Qy   1023  TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA  1082
           ||||| || |||||| |||||||||||| |||||| || ||| ||||||| |||| ||
Db   1069  TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC  1128

Qy   1083  CTCCAGATG  1091
           | | | |
Db   1129  TTACTCAAG  1137
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RESULT 10
US-09-954-456-1621
; Sequence 1621, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1621
;   LENGTH: 3088

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-1621

    Query Match          35.4%;   Score 449.4;  DB 3;   Length 3088;
    Best Local Similarity  71.5%;   Pred. No. 6.8e-122;
    Matches  607;  Conservative    0;  Mismatches 236;  Indels    6;  Gaps    1;

Qy        243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
              ||||  |||||| ||  |  |     ||||| |  |-||||||||||||  |||| |||||
Db        295 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy        303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
              |||  |||||||||| || | |||||| || |  |||||||||| | |    |||||| |
Db        355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy        363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
              ||||||||| | | ||| | ||||| ||||| || ||  ||         || |  | |||
Db        415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy        423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
              || |||| | |       | || ||||||||||| |||||| || || |||||| |   |
Db        475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy        483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
              | |  |  |   |    ||||||||| |||||||||||||||||||| || ||||||||||
Db        535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy        543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
              || |||||| |    |||||||||||||||||||||||| | ||| | |||||||| | |
Db        595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy        603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
              ||| |       | || |    | ||| ||| || || |||||||| || ||||||||
Db        655 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy        663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
              || ||||| |||||||||| | | ||| ||||| ||            |||||||||||||  |||
Db        709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy        723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
              | || |||||| ||||||||   |||||||||||||||||||||| || || ||| | ||||
Db        769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy        783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
              |||||||||||| || ||||||| ||||| ||| ||| |||||||| |||||||| || ||
Db        829 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACGGTGAT 888

Qy        843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
              ||| | ||||||||||||||||| |||| | | || |||| || ||||| || ||
Db        889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy        903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
              |||||  ||||||||||||||||||||| || ||||| |||||||||||| |||||| |
Db        949 CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG 1008

Qy        963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
              || |||||| ||||||||| |||| || |  |||||| |||    |||    |||||| | |||
Db       1009 GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC 1068

Qy       1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
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                  IIIII  II IIIII  IIIIIIIIIII IIIIII   II III   IIIIII IIII II
Db    1069 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy    1083 CTCCAGATG 1091
                I I  I I
Db    1129 TTACTCAAG 1137
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RESULT 11
US-09-969-347-234
; Sequence 234, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
;   APPLICANT: Ebner, Reinhard
;   TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
;   TITLE OF INVENTION: Sets
;   FILE REFERENCE: 689290-69
;   CURRENT APPLICATION NUMBER: US/09/969,347
;   CURRENT FILING DATE: 2001-10-02
;   PRIOR APPLICATION NUMBER: US/60/237,598
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: US/60/237,604
;   PRIOR FILING DATE: 2000-10-03
;   NUMBER OF SEQ ID NOS: 318
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 234
;   LENGTH: 3088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-969-347-234

    Query Match   35.4%;   Score 449.4; DB 3;   Length 3088;
    Best Local Similarity   71.5%;   Pred. No. 6.8e-122;
    Matches 607; Conservative   0; Mismatches 236; Indels   6; Gaps   1;

Qy   243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
               IIII IIIII II I I   IIIII I IIIIIIIIIIIIII IIII IIIII
Db   295 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy   303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
               III   IIIIIIII II I IIIIII II I IIIIIIIIII I I   IIIIII I
Db   355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy   363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
               IIIIIIIIII I III I IIIIII IIIII II III   II   I III
Db   415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy   423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
               II IIIII I I   I II IIIIIIIIII IIIII II IIIIII   I
Db   475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy   483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
               I I   I   I   IIIIIIIII IIIIIIIIIIIIIIIIIII IIIIIIIIIIII
Db   535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy   543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
               II IIIIII I   IIIIIIIIIIIIIIIIIIIIIII I III I IIIIIIIII I I
Db   595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy   603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
               III I   I II I   I III III II IIIIIII II IIIIIIIII
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Db        655 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy        663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
                || |||||| |||||||| | | ||| |||||| ||      |||||||||||||||| |||
Db        709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy        723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
                | || |||||| ||||||||| ||||||||||||| || || |||    ||| | ||||
Db        769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy        783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
                |||||||||| || ||||||| ||||| ||| |||||||| ||||||||| || ||
Db        829 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACGGTGAT 888

Qy        843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
                ||| | |||||||||||||||    |||| | | || |||| || |||||| || ||
Db        889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy        903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
                ||||| |||||||||||||||||||||||ꞁ|||| || ||||| |||||||||| ||||| |
Db        949 CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG 1008

Qy        963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
                || ||||| |||||||||| |||| || | ||||||| |||   ||| |||||| || |||
Db       1009 GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC 1068

Qy       1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
                ||||| || ||||| |||||||||||| |||||| || ||| |||||| |||| ||
Db       1069 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy       1083 CTCCAGATG 1091
                | |  | |
Db       1129 TTACTCAAG 1137
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RESULT 12
US-10-843-641A-3072
; Sequence 3072, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007

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;   PRIOR FILING DATE: 2001-10-02
;   PRIOR APPLICATION NUMBER: US/09/969,347
;   PRIOR FILING DATE: 2001-10-02
;   PRIOR APPLICATION NUMBER: US/09/969,708
;   PRIOR FILING DATE: 2001-10-03
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 8447
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3072
;   LENGTH: 3088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-843-641A-3072
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   Query Match              35.4%;   Score 449.4;   DB 10;   Length 3088;
   Best Local Similarity    71.5%;   Pred. No. 6.8e-122;
   Matches  607;  Conservative    0;  Mismatches  236;  Indels    6;  Gaps    1;

Qy        243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
              ||||  |||||  ||   |    |     ||||| | ||||||||||||||| |||| |||||
Db        295 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy        303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
              |||   ||||||||  || | ||||| || |  ||||||||||| | |     ||||||  |
Db        355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy        363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
               ||||||||||| | ||| | |||||| ||||| || |||      ||      | |||
Db        415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy        423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
              || ||||  | |     | ||  |||||||||||| |||||  || ||||| |
Db        475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy        483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
              | |   |   |    | ||||||||| |||||||||||||||||||||||| |||||||||||
Db        535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy        543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
              || |||||| |    |||||||||||||||||||||||| | ||| | |||||||||  | |
Db        595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy        603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
              |||  |         | || |     |   ||| || || |||||||| || ||||||||
Db        655 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy        663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
              || ||||| |||||||| | | ||| ||||| ||             |||||||||||||   |||
Db        709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy        723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
               | || ||||| ||||||| ||||||||| |||||||||||| || || |||   ||| | ||||
Db        769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy        783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
              ||||||||||| || ||||||| ||||| ||| ||||||| ||||||||| || ||
Db        829 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACGGTGAT 888

Qy        843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
              ||| | ||||||||||||||| ||||  | | | ||  |||| || ||||| || ||
Db        889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948
```

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Qy     903  CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
            |||||  |||||||||||||||||||||||  || |||||   |||||||||| |||||  |
Db     949  CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG 1008

Qy     963  GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
            ||  |||||| ||||||||| |||| || |  ||||||  |||    |||   ||||| || |||
Db    1009  GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC 1068

Qy    1023  TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
            |||||  || |||||  |||||||||||||  ||||||   || |||     |||||| |||| ||
Db    1069  TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy    1083  CTCCAGATG 1091
            |  |   | |
Db    1129  TTACTCAAG 1137
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RESULT 13.
US-10-843-641A-4648
; Sequence 4648, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4648
;   LENGTH: 3088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-843-641A-4648

     Query Match   35.4%;   Score 449.4;   DB 10;   Length 3088;
     Best Local Similarity   71.5%;   Pred. No. 6.8e-122;
      Matches 607; Conservative   0; Mismatches 236; Indels   6; Gaps   1;
```

```
Qy    243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
          ||||  |||||  || |   |     |||||  | |||||||||||||||  |||| ||||||
Db    295 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy    303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
          |||    ||||||||  || | ||||| || |  ||||||||||| | |    |||||| |
Db    355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy    363 GTCCTGGCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
          ||||||||||  | ||| | ||||| ||||| || ||| ||          |  |||
Db    415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy    423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
          ||  |||| | |     |  || ||||||||||||  ||||| ||||| ||  |||||| |
Db    475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy    483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
          | |   |    |    |||||||||| ||||||||||||||||||||| |||||||||||||
Db    535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy    543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
          ||  ||||||| |   ||||||||||||||||||||| | ||| | ||||||||||   | |
Db    595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy    603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
          ||| |        | ||| |   |   ||| ||| ||  |||||||| || ||||||||||
Db    655 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy    663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
          || ||||| |||||||||| |  | |  ||||| ||           |||||||||||| |||
Db    709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy    723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
          | || |||||| ||||||||  |||||||||||||||| || || ||| ||| | ||||
Db    769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy    783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
          ||||||||||||| ||  |||||||||  |||||  ||| ||| |||||||| |||||||| || ||
Db    829 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACGGTGAT 888

Qy    843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
          ||| | ||||||||||||||||||           |||| | | || |||  || ||||| || ||
Db    889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy    903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
          |||||  ||||||||||||||||||||||||| || ||||| |  ||||||||| |||||  |
Db    949 CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG 1008

Qy    963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
          || |||||| |||||||||| |  || | |||||||| |||     ||| ||||| || |||
Db   1009 GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC 1068

Qy   1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
          |||||  || |||||||||| ||||||||||||| |||||   || ||| |||||| ||| ||
Db   1069 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy   1083 CTCCAGATG 1091
          |   |   |
Db   1129 TTACTCAAG 1137
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RESULT 14
US-10-843-641A-8363
; Sequence 8363, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;. APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8363
;   LENGTH: 3088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-843-641A-8363

   Query Match               35.4%;  Score 449.4;  DB 10;  Length 3088;
   Best Local Similarity     71.5%;  Pred. No. 6.8e-122;
   Matches  607;  Conservative    0;  Mismatches 236;  Indels    6;  Gaps    1;

Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
                ||||   |||||| ||  |   |     |||||  | |||||||||||||| |||| |||||
Db      295 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
                |||   ||||||||| || | ||||| || |  |||||||||| | |     |||||| |
Db      355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy      363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
                |||||||||| | ||| | ||||| ||||| || |||         ||      | |||
Db      415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
                || |||| | |       | ||  ||||||||||||| |||||  || ||||||    |
Db      475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534
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Qy      483  GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
                | |   |    |      ||||||||| |||||||||||||||||||| |||||||||||
Db      535  GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy      543  GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
                || ||||||| |   ||||||||||||||||||||| | ||| | ||||||||| | |
Db      595  CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy      603  CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
                ||| |        | || |    |   ||| ||| || ||||||| || |||||||||
Db      655  CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy      663  GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
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; Sequence 275, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS A
;  TITLE OF INVENTION:  METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/756,149
;  CURRENT FILING DATE:  2004-01-12
;  NUMBER OF SEQ ID NOS: 5818
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
;   LENGTH: 3088
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;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-10-756-149-275

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     Best Local Similarity  71.5%;    Pred. No. 6.8e-122;
     Matches  607;  Conservative    0;  Mismatches 236;  Indels    6;  Gaps    1;

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Job time : 1819 secs

SCORE 1.3   BuildDate: 12/06/2005

SCORE Search Results Details for Application 09844268 and Search Result us-09-844-268-12.rnpbn.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 09844268 and Search Result us-09-844-268-12.rnpbn.

start

Go Back to previous page

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                    GenCore version 5.1.9
          Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:           November 13, 2006, 21:00:21 ; Search time 350 Seconds
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Searched:         2471159 seqs, 989689746 residues

Total number of hits satisfying chosen parameters:      4942318

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
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	2	449.4	35.4	3088	8	US-11-266-748A-56661	Sequence 56661, A
	3	447.8	35.3	1784	8	US-11-266-748A-61104	Sequence 61104, A
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	5	371.2	29.3	1076	8	US-11-266-748A-126696	Sequence 126696,
c	6	210	16.5	1000	8	US-11-266-748A-210852	Sequence 210852,
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ALIGNMENTS

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US-11-266-748A-28779
; Sequence 28779, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick

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;  APPLICANT:  Mulligan,  Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28779
;   LENGTH: 3088
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
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          ||| | |||||||||||||||||||||  |||| | | || |||| || ||||| || ||
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RESULT 2
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; Sequence 56661, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;   APPLICANT: Harkin, Paul
;   APPLICANT: Johnston, Patrick
;   APPLICANT: Mulligan, Karl
;   TITLE OF INVENTION: Transcriptome Microarray Technology and
;   TITLE OF INVENTION: Methods of Using the Same
;   FILE REFERENCE: 55815-0102 (319189)
;   CURRENT APPLICATION NUMBER: US/11/266,748A
;   CURRENT FILING DATE: 2005-11-03
;   PRIOR APPLICATION NUMBER: EP 04105479.2
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105482.6
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105483.4
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;   PRIOR FILING DATE: 2005-07-18
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;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56661
;   LENGTH: 3088
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;   ORGANISM: Homo Sapiens
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             | |  | |   |        ||||||||| |||||||||||||||||||||||| |||||||||||
Db       535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy       543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
             || ||||||| |   |||||||||||||||||||||||||| | ||| | ||||||||| | |
Db       595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy       603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
             ||| |         | || |      |   | |  ||| || ||||||| || ||||||||
Db       655 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy       663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
             || ||||| |||||||||| | | | ||| |||||| ||     ||||||||||||||| |||
Db       709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy       723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCTTT 782
             |  || |||||| |||||| |||||||||| |||||||||||||| || || |||   ||| | ||||
Db       769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy       783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCGGGGGGGAC 842
             |||||||||||| || ||||||| ||||| ||| || |||||| ||||||||||  || ||
Db       829 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACGGTGAT 888

Qy       843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
             ||| | ||||||||||||||||||    |||| | | || |||| || ||||| || ||
Db       889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy       903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
             ||||| |||||||||||||||||||||||| || ||||| |||||||||||| ||||| |
Db       949 CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG 1008
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```
Qy    963  GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
           ||  ||||||  |||||||||  ||||  ||  |  |||||||  |||    |||    |||||  ||  |||
Db   1009  GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC 1068

Qy   1023  TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
           |||||  ||  ||||||  ||||||||||||  ||||||    ||  |||    ||||||  ||||  ||
Db   1069  TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy   1083  CTCCAGATG 1091
            |  |   |   |
Db   1129  TTACTCAAG 1137
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RESULT 3
US-11-266-748A-61104
; Sequence 61104, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61104
;   LENGTH: 1784
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-61104

  Query Match   35.3%; Score 447.8; DB 8; Length 1784;
  Best Local Similarity 71.4%; Pred. No. 7.1e-101;
  Matches 606; Conservative   0; Mismatches 237; Indels   6; Gaps   1;

Qy   243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
           |||| |||||| || | || ||||| | ||||||||||||||| |||| |||||
Db   245 GGGATGTGGACGATCAATGCGATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 304

Qy   303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
           ||| |||||||| || | ||||| ||| | ||||||||||| | | |||||| |
```

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Db    305 CTGTATGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 364

Qy    363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
              |||||||||| | ||| | |||||  |||||  ||  |||        ||      | |||
Db    365 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 424

Qy    423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
              || |||| ||     | ||  ||||||||||  |||||  ||  ||||  |     |
Db    425 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACATCCCG 484

Qy    483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
              | |     | |   | ||||||||| ||||||||||||. |||||||| ||||||||||||
Db    485 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGC 544

Qy    543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
              || ||||||  | |||||||||||||||||||||||||||| | ||| | |||||||||  | |
Db    545 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 604

Qy    603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
              ||| |        | || |     |  ||| ||| ||  |||||||| || |||||||||
Db    605 CTGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 658

Qy    663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
              || ||||| |||||||||| | | ||| |||||| || |||||||||||||||||||| |||
Db    659 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 718

Qy    723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCTTT 782
              | || ||||| |||||||||||  ||||||||||||||| || || ||    ||| | ||||
Db    719 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 778

Qy    783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCGGGGGGGAC 842
              |||||||||| || ||||||  ||||| ||| ||||||| |||||||||| | ||
Db    779 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACAGTGAT 838

Qy    843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
              ||| | |||||||||||||||||    |||| | | || |||| || ||||| || ||
Db    839 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 898

Qy    903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
              ||||| ||||||||||||||||||||||||  | ||||     |||||||||| ||||| |
Db    899 CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCCGCATACCTCACG 958

Qy    963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
              || ||||| |||||||||| || | | |||||| |||       ||| ||||| || |||
Db    959 GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCCTCAAAATC 1018

Qy   1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
              ||||| || ||||| |||||||||||| ||||||  ||| ||      |||||| |||| ||
Db   1019 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACGGGGATTGCCGCAGACCTGTCCCCC 1078

Qy   1083 CTCCAGATG 1091
              |  | | ||
Db   1079 TTACTCAAG 1087
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RESULT 4
US-11-266-748A-73885/c
; Sequence 73885, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul

```
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73885
;   LENGTH: 1076
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-73885
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    Query Match          29.3%;  Score 371.2;  DB 8;  Length 1076;
    Best Local Similarity  70.5%;  Pred. No. 5.2e-82;
    Matches  512;  Conservative    0;  Mismatches  208;  Indels   6;  Gaps    1;

Qy         243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
               ||||  ||||||  ||   | ||    |||||  | |||||||||||||||  |||| |||||
Db         782 GGGATGTGGACGATCAATGCGATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 723

Qy         303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
               |||    ||||||||  || | ||||| || |  ||||||||||| | |     |||||| |
Db         722 CTGTATGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 663

Qy         363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
                |||||||||| | ||| | ||||| ||||| || ||| |     ||     | |||
Db         662 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 603

Qy        ·423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
               || |||| | |     | || ||||||||||||  |||||| ||   |||| |    |
Db         602 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACATCCCG 543

Qy         483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
                | |  |   |     |||||||||| |||||||||| |||||||| ||||||||||||||||
Db         542 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGC 483

Qy         543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
               || |||||| |   |||||||||||||||||||||||||| | ||| | |||||||| | |
Db         482 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 423

Qy         603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
               ||| |        | || |     | ||| ||| ||  |||||||| || ||||||||||
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```
Db      422 CTGCGGG------GCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 369

Qy      663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
                ||  |||||| |||||||||  |  |  ||| |||||  ||       ||||||||||||||||||   |||
Db      368 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 309

Qy      723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
               |  || |||||  |.|||||||||  |||||||||||||  ||  ||  |||       |||  |  ||||
Db      308 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 249

Qy      783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
               ||||||||||||  |||  |||||||||  ||||||  |||  |||||||||  ||||||||||    .|  ||
Db      248 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACAGTGAT 189

Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
               |||. |  |||||||||||||||||       ||||  |  |  ||  ||||   ||  |||||| ||  ||
Db      188 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 129

Qy      903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
               |||||  ||||||||||||||||||||||||||||||||||  ||  ||  ||  ||||||||||  |||||    |
Db      128 CAGTGTAACCACACCATCATGACCATTGGGACGTTGGGGATCTGGGCCGCATACCCCTCG 69

Qy      963 GGTGGA 968
               ||  ||
Db       68 TGTTGA 63
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RESULT 5
US-11-266-748A-126696
; Sequence 126696, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126696
;   LENGTH: 1076
;   TYPE: DNA
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;    ORGANISM: Homo Sapiens
US-11-266-748A-126696

    Query Match            29.3%;   Score 371.2;  DB 8;   Length 1076;
    Best Local Similarity  70.5%;   Pred. No. 5.2e-82;
    Matches  512;  Conservative   0;  Mismatches 208;  Indels    6;  Gaps     1;

Qy        243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
              ||||  |||||  ||   |  ||     |||||  ||||||||||||||| |||| |||||
Db        295 GGGATGTGGACGATCAATGCGATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 354

Qy        303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
              |||    ||||||||  ||| | ||||| || |  |||||||||||| | |    ||||||  |
Db        355 CTGTATGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy        363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
              ||||||||| | | ||| | |||||| ||||| ||  |||       ||      | |||
Db        415 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy        423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
               || |||| | |      | || |||||||||||  ||||| ||  |||| |  |  |  |
Db        475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACATCCCG 534

Qy        483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
               | |   |   |    |||||||||| ||||||||||| |||||| |||||| |||||||||
Db        535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGC 594

Qy        543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
               || |||||| |  |||||||||||||||||||||||| |  |||  | |||||||| | |
Db        595 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTC 654

Qy        603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
              ||| |        | || |    |   ||| || | |||||||| || || ||||||||
Db        655 CTGCGGG------GCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy        663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
              || |||||  ||||||||| | | |||  |||||  || |||||||||||||||||  |||
Db        709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy        723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782
               | || |||||| ||||||||  ||||||||||||||||||| || || |||   | ||||
Db        769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy        783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
              |||||||||||| || ||||||| ||||| ||| ||| |||||||| |||||||||  | ||
Db        829 GTGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACATTGACACCTCCCACAGTGAT 888

Qy        843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
              ||| | |||||||||||||| |||| | | || || |||| || ||||| || || ||
Db        889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy        903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
              ||||| |||||||||||||||||||||||  || || ||  |||||||||| ||||    |
Db        949 CAGTGTAACCACACCATCATGACCATTGGGACGTTGGGGATCTGGGCCGCATACCCCTCG 1008

Qy        963 GGTGGA 968
              ||  ||
Db       1009 TGTTGA 1014
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RESULT 6

US-11-266-748A-210852/c
; Sequence 210852, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 210852
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-210852

     Query Match   16.5%; Score 210; DB 8; Length 1000;
     Best Local Similarity 69.1%; Pred. No. 3.7e-42;
     Matches 318; Conservative   0; Mismatches 135; Indels   7; Gaps   2;

Qy   365 CCTGGCCCCCGTGTTCCGCAT-CACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCACG 423
              |||||||||| | ||| | || ||| ||||| || || || |||
Db   454 CCTGGCCCCCATCTTCAGAATCCACCCTGCCGGTGGTGCAAAGCGCCACGTCCAGCAGGA 395

Qy   424 CTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGG 483
              || ||||| || | | || ||| ||||||| ||||| || |||| | | ||
Db   394 TCCCCTGGCAGAACTACCACCTGAACGTCTGGATGGAGGAGGAATACCGCCACATCCCGG 335

Qy   484 AGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGG 543
                | | | ||||||||| |||||||||| |||||||| |||||||||||
Db   334 GGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGCC 275

Qy   544 AGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTAC 603
              || ||||| | ||||||||||||||||||||||| | ||| | |||||||| | | |
Db   274 AGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCCAGAAGTTCC 215

Qy   604 TGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACG 663
              || | | || | | ||| ||| || || ||||||| || |||||||| |
Db   214 TGCG------GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCATG 161

Qy   664 TGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACG 723

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                  | |||||| ||||||||| | | ||| ||||| ||    ||||||||||||||||| |||
Db      160 TTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGACC 101

Qy      724 GCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTG 783
                  | || ||||| ||||||||| ||||||||||||| || || |||    ||| | ||||| |
Db      100 GGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTCG 41

Qy      784 TGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACAT 823
                  ||||||||||| || ||||||| ||||| ||| |||||||
Db       40 TGGTCACCAGTAATGGCATGGCCTGGTGTCGGGAGAACAT 1
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RESULT 7
US-11-266-748A-369805
; Sequence 369805, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; .PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 369805
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-369805

   Query Match   8.0%;   Score 101.6; DB 8;   Length 807;
   Best Local Similarity   63.5%;   Pred. No. 2.2e-15;
   Matches 188; Conservative   0; Mismatches 104; Indels   4; Gaps   2;

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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
                  |||| ||||| || | |    ||||| | ||||||||||||||| |||| ||||||
Db      266 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 325

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
                  |||     ||||||||| || | ||||| || | ||||||||| | |    |||||| |
Db      326 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 385
```

```
Qy    363 GTCCTGGCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
          |||||||||||| | ||| | |||||| ||||| || |||     || |   | |||
Db    386 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 445

Qy    423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
          || |||| | |       | || ||||||||||| | | || ||    |||| |     |
Db    446 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGGAGAATACCGCCACCTCCCG 505

Qy    483 GAGCCCT--GGCTGAAGCTCACCGGCTT--CCCCTGCTCCTGGACCTTCTTCCACC 534
          | |   |  | ||  |||||||| | ||| |||||| ||||||||| |||||
Db    506 GGGGGATTACGTTCCGCTTCACCGGCCTACCCCTGGCTCCTAGACCTTCTACCACC 561
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RESULT 8
US-11-266-748A-453184/c
; Sequence 453184, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 453184
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-453184

  Query Match   8.0%;   Score 101.6; DB 8; Length 807;
  Best Local Similarity   63.5%;   Pred. No. 2.2e-15;
  Matches 188; Conservative   0; Mismatches 104; Indels   4; Gaps   2;

Qy   243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
          |||| ||||| || | | | ||||| | ||||||||||||||||| |||| |||||
Db   542 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA 483

Qy   303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
          ||| |||||||| || | ||||| || | ||||||||||| | | |||||| |
Db   482 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 423
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```
Qy    363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
          ||||||||||| | ||| | ||||| ||||| || |||      ||      | |||
Db    422 ACCCTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 363


Qy    423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
          || |||| || || |||| |||||||||| | || ||  |||| |  |
Db    362 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGGAGAATACCGCCACCTCCCG 303


Qy    483 GAGCCCT--GGCTGAAGCTCACCGGCTT--CCCCTGCTCCTGGACCTTCTTCCACC 534
          | |   |  | |  |||||||| | ||| ||||||| ||||||||| |||||
Db    302 GGGGGATTACGTTCCGCTTCACCGGCCTACCCCTGGCTCCTAGACCTTCTACCACC 247



RESULT 9
US-10-561-201-3/c
; Sequence 3, Application US/10561201
; Publication No. US20060211115A1
; GENERAL INFORMATION:
;  APPLICANT: The Trustees of the University of Pennsylvania
;  APPLICANT:  Roy, Soumitra
;  APPLICANT:  Wilson, James M.
;  TITLE OF INVENTION: Methods of Generating Chimeric Adenoviruses and Uses For Such
;  TITLE OF INVENTION:  Chimeric Adenoviruses
;  FILE REFERENCE: UPN-P3067PCT
;  CURRENT APPLICATION NUMBER: US/10/561,201
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: US 10/465,302
;  PRIOR FILING DATE: 2003-06-20
;  PRIOR APPLICATION NUMBER: US 60/566,212
;  PRIOR FILING DATE: 2004-04-28
;  PRIOR APPLICATION NUMBER: US 60/575,429
;  PRIOR FILING DATE: 2004-05-28
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 36535
;   TYPE: DNA
;   ORGANISM: chimpanzee adenovirus serotype Pan7
US-10-561-201-3


  Query Match              3.8%;   Score 48.6;  DB 6;  Length 36535;
  Best Local Similarity   54.1%;   Pred. No. 0.11;
  Matches   99; Conservative   0;  Mismatches   84;  Indels    0;  Gaps    0;

Qy    773 CCCCGTCTTTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTC 832
          | || |  ||||| ||| || || | |||| || | | | ||| | ||| | ||
Db   7852 CACCTACGATGTGGAAACCTACACCTGGATGGGGTCCTTCGGCAAGCAGCTCGTCCCCTT 7793


Qy    833 CCGGGGGGACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGC 892
          | . | || | ||| | ||| || || || | | | ||| || |||| ||| | ||
Db   7792 CATGCTGGTCATGAAACTCTCCGGGGACCCGCCGCTCGTCGAGCTCGCCCACGACCTCGC 7733


Qy    893 GCTGCTGGTGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGC 952
          || | | |||| ||| |     |     |   ||||||||| || |     || |
Db   7732 CCTCCAGCTCAAGTGGGACCGCTGGCACGGCGACCCCCGCACCTTCTACTGCGTCACCCC 7673


Qy    953 CTA 955
          | |
Db   7672 CGA 7670
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RESULT 10
US-10-561-201-2/c
; Sequence 2, Application US/10561201
; Publication No. US20060211115A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Roy, Soumitra
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Methods of Generating Chimeric Adenoviruses and Uses For Such
; TITLE OF INVENTION: Chimeric Adenoviruses
; FILE REFERENCE: UPN-P3067PCT
; CURRENT APPLICATION NUMBER: US/10/561,201
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: US 10/465,302
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/566,212
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US 60/575,429
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 36604
;   TYPE: DNA
;   ORGANISM: chimpanzee adenovirus serotype Pan6
US-10-561-201-2

    Query Match   3.8%;   Score 48.6; DB 6; Length 36604;
    Best Local Similarity   54.1%;   Pred. No. 0.11;
    Matches   99; Conservative   0; Mismatches   84; Indels   0; Gaps   0;

Qy   773 CCCCGTCTTTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTC 832
                | || | ||||| ||| || | | |||| || | | | ||| | ||| | |||
Db   7846 CACCTACGATGTGGAAACCTACACCTGGATGGGGTCCTTCGGCAAGCAGCTCGTCCCCTT 7787

Qy   833 CCGGGGGGACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGC 892
                | | || | ||| | | | || || || | | || || |||| ||| | ||
Db   7786 CATGCTGGTCATGAAACTCTCCGGGGACCCGCCGCTCGTCGAGCTCGCCCACGACCTCGC 7727

Qy   893 GCTGCTGGTGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGC 952
                 || | | | |||| ||| | | | |||||||| || | || |
Db   7726 CCTCCAGCTCAAGTGGGACCGCTGGCACGGCGACCCCCGCACCTTCTACTGCGTCACCCC 7667

Qy   953 CTA 955
                | |
Db   7666 CGA 7664

RESULT 11
US-11-218-305-13034
; Sequence 13034, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B

```
;   CURRENT APPLICATION NUMBER: US/11/218,305
;   CURRENT FILING DATE:  2005-09-01
;   PRIOR APPLICATION NUMBER: US 60/606,880
;   PRIOR FILING DATE: 2004-09-01
;   NUMBER OF SEQ ID NOS: 25043
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13034
;   LENGTH: 6573
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (214)..(214)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1342)..(1342)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3788)..(3788)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5035)..(5035)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5217)..(5217)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-13034

   Query Match              3.7%;  Score 47.4;  DB 9;  Length 6573;
   Best Local Similarity   48.0%;  Pred. No. 0.12;
   Matches  135;  Conservative    0;  Mismatches  146;  Indels   0;  Gaps    0;

Qy        683 GCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGTTACCTCCAGCAGGC 742
              | |||||        | |  ||  |||||||| | |||||  |||    |   |  | | |
Db       2582 GTGTGTGGGTGTGGGGGGGCGGGGTGGGGTGGGGAGTGACACCCGGGGGCCGATGACGAC 2641

Qy        743 TATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTTGTGGTCACCAGCAACGGCAT 802
              || ||  |  || | |       || | |  ||  |||    ||||||  || | |
Db       2642 GCTGCACATGGACCCGCCGGCGCCGCCCGCGCGCCGCTCAGTGTCGACCAGCTGCGACCT 2701

Qy        803 GGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATCTTTGCTGGCGATGG 862
              | |   | || |||  || || |  || |    | |  | ||  |      | | ||
Db       2702 GCACCCGGGCGAGACGTTCACCGGCTTCTGCGCCGCGTGCCTGCGCGAGCGCCTCCACGG 2761

Qy        863 GCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGCAACCACACCATCAT 922
              |. |||||  |  ||||| | ||  |||| |  |  |   ||| ||      |||||
Db       2762 TCTCGAGGCGTCCGCCGCCGCCGCCTCCGCGCCGGGGCGCAAGTCCACATCGGCCATCCG 2821

Qy        923 GACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTG 963
              | ||| | | ||    |||    |||| |  |  | | ||| 
Db       2822 GTCCCTGTTCGCCAGGCCGTTCGCCGCCGGCAGCTCGTCTG 2862
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RESULT 12
US-10-561-201-1/c
; Sequence 1, Application US/10561201
; Publication No. US20060211115A1

```
;  GENERAL INFORMATION:
;   APPLICANT: The Trustees of the University of Pennsylvania
;   APPLICANT:  Roy, Soumitra
;   APPLICANT:  Wilson, James M.
;   TITLE OF INVENTION: Methods of Generating Chimeric Adenoviruses and Uses For Such
;   TITLE OF INVENTION:  Chimeric Adenoviruses
;   FILE REFERENCE: UPN-P3067PCT
;   CURRENT APPLICATION NUMBER: US/10/561,201
;   CURRENT FILING DATE:  2005-12-19
;   PRIOR APPLICATION NUMBER: US 10/465,302
;   PRIOR FILING DATE: 2003-06-20
;   PRIOR APPLICATION NUMBER: US 60/566,212
;   PRIOR FILING DATE: 2004-04-28
;   PRIOR APPLICATION NUMBER: US 60/575,429
;   PRIOR FILING DATE: 2004-05-28
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 1
;    LENGTH: 36462
;    TYPE: DNA
;    ORGANISM: chimpanzee adenovirus serotype Pan5
US-10-561-201-1

   Query Match              3.7%;   Score 47;  DB 6;   Length 36462;
   Best Local Similarity   53.6%;   Pred. No. 0.27;
   Matches   98;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy        773 CCCCGTCTTTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTC 832
              | ||  |    |||| |||  || | | |||| ||  | | ||| |  ||| | |||
Db       7840 CACCTACGACGTGGAAACCTACACCTGGATGGGGTCCTTCGGCAAGCAGCTCGTCCCCTT 7781

Qy        833 CCGGGGGGACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGC 892
              | |  || | ||| |  | | || ||  || |  | || || |||| |||  ||| | ||
Db       7780 CATGCTGGTCATGAAACTCTCCGGGGACCCGCCGCTCGTCGAGCTCGCCCACGACCTCGC 7721

Qy        893 GCTGCTGGTGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGC 952
              || | | |  |||| ||| |   |      |      | |||||||| || |    || |
Db       7720 CCTCCAGCTCAAGTGGGACCGCTGGCACGGCGACCCCCGCACCTTCTACTGCGTCACCCC 7661

Qy        953 CTA 955
              | |
Db       7660 CGA 7658


RESULT 13
US-11-218-305-24825/c
;  Sequence 24825, Application US/11218305
;  Publication No. US20060141495A1
;  GENERAL INFORMATION:
;   APPLICANT: MONSANTO TECHNOLOGY, LLC
;   APPLICANT:  McLaird, Paul L.
;   APPLICANT:  Tao, Nengbing
;   APPLICANT:  Wu, Kunsheng
;   TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;   TITLE OF INVENTION:  Corn.
;   FILE REFERENCE: 38-21 (53660)B
;   CURRENT APPLICATION NUMBER: US/11/218,305
;   CURRENT FILING DATE:  2005-09-01
;   PRIOR APPLICATION NUMBER: US 60/606,880
;   PRIOR FILING DATE: 2004-09-01
;   NUMBER OF SEQ ID NOS: 25043
```

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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24825
;   LENGTH: 1158
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (19)..(19)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (36)..(36)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-24825
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```
   Query Match              3.7%;  Score 46.6;  DB 9;  Length 1158;
   Best Local Similarity   48.3%;  Pred. No. 0.099;
   Matches  130;  Conservative   0;  Mismatches 139;  Indels    0;  Gaps    0;
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```
Qy     272 GTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTGGCCCTGGCGCAGCTCAACGGCCG 331
           ||| |||   |   |     |   |  | ||| ||| || ||| |   |||| |     | ||
Db     564 GTTCGGGCTCATGTACGCCTACTTTGCGACGGTGATGGACAAAGCGCGGAGGGTCCGCGC 505

Qy     332 CCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTGGCCCCCGTGTTCCGCATCACGCT 391
           |   |||        | | | ||  || |||||| |  || | |       || |  ||| 
Db     504 CGGCGCCGGAGCGCTGGCGGCGCCGCTCGCCGTGGGGCTCCTGGCGGGGGCCAACGTGCT 445

Qy     392 GCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCTTGGCGGGAGCTGGAGCTTCACGA 451
           | |   |   |||| |||| |  |   |   ||| ||| | | | | ||     || 
Db     444 GGCCTGCGGCGCGCTGGAGGGCGCCGTGATGAATCCGGCGCGCGCGTTCGGGCCCGCCGT 385

Qy     452 CTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCCTGGCTGAAGCTCACCGGCTTCCC 511
           | |   |||     |      ||| |  || | |||| || || || | |   | | 
Db     384 CGTGGGCTCCCGTCGCTGGAGACACCAATGGGTGTACTGGGTGGGGCCCATGGTCGGCGC 325

Qy     512 CTGCTCCTGGACCTTCTTCCACCACCTCC 540
           | || ||     | || || || | | ||
Db     324 CGGCCTCTCCGGCGTCGTCTACGAGCACC 296
```

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RESULT 14
US-11-056-355B-63909
; Sequence 63909, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 63909
;   LENGTH: 1196
```

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;    TYPE: DNA
;    ORGANISM: Triticum aestivum
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)..(1196)
;    OTHER INFORMATION: Ceres Seq. ID no. 12616895
US-11-056-355B-63909

     Query Match              3.7%;   Score 46.6;  DB 9;  Length 1196;
     Best Local Similarity   47.4%;   Pred. No. 0.1;
     Matches  174;  Conservative    0;  Mismatches 189;  Indels    4;  Gaps    1;

Qy        546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTACTG 605
              ||  ||| | |       || ||| |  | ||  || | ||||| || |    | | | |
Db        609 CATGTCCTCCGATCTCTCCCCCATCCAGTCCGGCTGCTGCAAGCCTCCGATCAGCTGCGG 668

Qy        606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
              |||  | | |||| ||  | | || ||||||| ||| ||    ||| || | || || ||
Db        669 CTTCACCTACGTCAACAGCACGCAATGGACCGGCCCCGCCAAGTCGACGGAGCCCGACTG 728

Qy        666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
              || ||||| || | |   || |         |  || | | | ||| || |       |
Db        729 CGGCGCGTGGTCCAACGACGGGGCGCTCTGCTACGGCTGCCAGTCGTGCAAGGCCGGCGT 788

Qy        726 CGTTACCTCCAGCAGGC----TATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTT 781
              ||  || || || ||      | | | | |   |       | | || | | | || |
Db        789 GGTGGCCACCCTCAAGCGCAATTGGAAGCGCTCCGCCATCATCAACATCGTCTTCCTCGT 848

Qy        782 TGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGA 841
              |  ||| ||     |   |   | ||| |   || |  ||| | ||| | ||       |
Db        849 CTTCATCATCATTGTCTACTCCGTCGGCTGCTGCGCCTTCAGGAACAACCGCCGCGACCA 908

Qy        842 CGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGT 901
              | | | | | ||  | || | | ||| |||| |||| ||||| |    |||| | | | |
Db        909 CCGCAACGGCGGCGGGTACAAGCAGCAGGGCGCGTACGCCTGATCGTTTGGCTCGGTTAT 968

Qy        902 GCAGTGC 908
              | |||
Db        969 TTATTGC 975


RESULT 15
US-11-218-305-24824/c
; Sequence 24824, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24824
;    LENGTH: 1217
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;    TYPE: DNA
;    ORGANISM: Zea mays
US-11-218-305-24824

    Query Match            3.5%;   Score 45;   DB 9;   Length 1217;
    Best Local Similarity  48.0%;  Pred. No. 0.25;
    Matches  129;  Conservative   0;  Mismatches 140;  Indels   0;  Gaps   0;

Qy        272 GTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTGGCCCTGGCGCAGCTCAACGGCCG 331
              ||| |||   |   |     |  | ||| ||| || ||| |    |||| |      | ||
Db        599 GTTCGGGCTCATGTACGCCTACTTTGCGACGGTGATGGACAAAGCGCGGAGGGTCCGCGC 540

Qy        332 CCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTGGCCCCCGTGTTCCGCATCACGCT 391
              |   |||     | | | ||  || |||||||   |   | |      || |   |||
Db        539 CGGCGCCGGAGCGCTGGCGGCGCCGCTCGCCGTGGGGCTTCTGGCGGGGGGCCAACGTGCT 480

Qy        392 GCCTGTCCTGGCGCCCGAGGTAGACAGGCACGCTCCTTGGCGGGAGCTGGAGCTTCACGA 451
              | |   |   |||| |||| | | |   |||   ||| | | | || | |   | | ||
Db        479 GGCCTGCGGCGCGCTGGAGGGCGCCGTGATGAATCCGGCGCGCGCGTTCGGGCCCGCCGT 420

Qy        452 CTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCCTGGCTGAAGCTCACCGGCTTCCC 511
              | |   |||      |     ||| | || | || | |||| || || || || | | |
Db        419 CGTGGGCTCCCGTCGCTGGAGACACCAATGGGTGTACTGGGTGGGGCCCATGGTCGGCGC 360

Qy        512 CTGCTCCTGGACCTTCTTCCACCACCTCC 540
              | || ||    | || || || | | ||
Db        359 CGGCCTCTCCGGCGTCGTCTACGAGCACC 331


Search completed: November 14, 2006, 02:47:14
Job time : 353 secs
```

SCORE 1.3   BuildDate: 12/06/2005